SEQUENCE LISTING

<110> CODEXIS, INC.

<120> ENGINEERED GLYCOSYLTRANSFERASES AND STEVIOL GLYCOSIDE GLUCOSYLATION METHODS

<130> CX8-163WO3

<140> NOT YET ASSIGNED
<141> SUBMITTED HEREWITH

<150> US 62/454,417
<151> 2017-02-03

<150> US 62/479,262
<151> 2017-03-30

<160> 9240

<210> 1
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 wild type

<400> 1
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ttcagtatca ccatctttca caccaacttc aacaaaccca aaacatctaa ttaccctcac 180
ttcactttca gattcatcct cgacaacgac ccacaagacg aacgcatttc caatctaccg 240
actcatggtc cgctcgctgg tatgcggatt ccgattatca acgaacacgg agctgacgaa 300
ttacgacgcg aactggaact gttgatgtta gcttctgaag aagatgaaga ggtatcgtgt 360
ttaatcacgg atgctctttg gtacttcgcg caatctgttg ctgacagtct taacctccga 420
cggcttgttt tgatgacaag cagcttgttt aattttcatg cacatgtttc acttcctcag 480
tttgatgagc ttggttacct cgatcctgat gacaaaaccc gtttggaaga acaagcgagt 540
gggtttccta tgctaaaagt gaaagacatc aagtctgcgt attcgaactg gcaaatactc 600
aaagagatat tagggaagat gataaaacaa acaagagcat cttcaggagt catctggaac 660
tcatttaagg aactcgaaga gtctgagctc gaaactgtta tccgtgagat cccggctcca 720
agtttcttga taccactccc caagcatttg acagcctctt ccagcagctt actagaccac 780
gatcgaaccg tttttcaatg gttagaccaa caaccgccaa gttcggtact gtatgttagt 840
tttggtagta ctagtgaagt ggatgagaaa gatttcttgg aaatagctcg tgggttggtt 900
gatagcaagc agtcgttttt atgggtggtt cgacctgggt ttgtcaaggg ttcgacgtgg 960
gtcgaaccgt tgccagatgg gttcttgggt gaaagaggac gtattgtgaa atgggttcca 1020
cagcaagaag tgctagctca tggagcaata ggcgcattct ggactcatag cggatggaac 1080
tctacgttgg aaagcgtttg tgaaggtgtt cctatgattt tctcggattt tgggctcgat 1140
caaccgttga atgctagata catgagtgat gttttgaagg taggggtgta tttggaaaat 1200
gggtgggaaa gaggagagat agcaaatgca ataagaagag ttatggtgga tgaagaagga 1260
gaatacatta gacagaatgc aagagttttg aaacaaaagg cagatgtttc tttgatgaag 1320
ggtggt 1326

<210> 2

<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 wild type

<400> 2
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn

370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly
435 440

<210> 3
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized UGT76G1

<400> 3
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ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 4
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 wild type

<400> 4
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile

1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445

Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 5
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ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtggagggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 6
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 6
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60

Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 7
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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 8
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 8
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
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Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 9
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 9
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ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtatgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggtgccg 1020
caacaagaag ttctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaat 1080
ggcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 10
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 10
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175

Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 11
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 11
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480

tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtggagtgtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 12
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 12
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro

225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Ser Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 13
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 13
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtatgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900

gacagcaaac aaagctttgt gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggtgccg 1020
caacaagaag ttctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaat 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 14
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 14
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285

Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Val Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 15
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 15
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcacga ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320

ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 16
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 16
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala

340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 17
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 17
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtggttggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 18
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 18
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400

Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 19
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 19
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gttggttagc 840
tttggcagca taagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt ggtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggcgccg 1020
caacaagaag ttctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggggt 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 20
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 20
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15

Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Leu Val Ser Phe Gly Ser Ile Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Gly Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Ala Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Gly Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 21
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 21
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtggaatgtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 22
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 22
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro

65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Asn Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 23
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 23
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatctgaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 24
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 24
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125

Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Leu Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 25
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 25
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120

tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtatgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggcgccg 1020
caacaagaag ttctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaat 1080
ggcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 26
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 26
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser

180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Ala Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 27
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 27
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540

ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtatgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggtgccg 1020
caacaagaaa ttctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaat 1080
ggcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 28
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 28
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240

Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Ile Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 29
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 29
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtc gtatcattct gtttccggtt 60
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 120
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 180
ttcacctttc gtttcatcct ggacaacgat ccgcaggacg agcgtattag caacctgccg 240
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 300
ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 360
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 420
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaaggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcggtgt gatttggaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcctga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gataagaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggtctggtt 900
gacagcaaac aaagctttct gtgggtggtt cgtccgggct tcgtgaaggg tagcacctgg 960

gttgagccgc tgccggatgg ttttctgggc gaacgtggtc gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggacccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggtctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374

<210> 30
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Variant

<400> 30
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1 5 10 15
Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20 25 30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35 40 45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50 55 60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65 70 75 80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85 90 95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
100 105 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
115 120 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
130 135 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145 150 155 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
165 170 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
180 185 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
195 200 205
Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
210 215 220
Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
225 230 235 240
Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
245 250 255
Leu Leu Asp His Asp Lys Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
260 265 270
Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
275 280 285
Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln

290 295 300
Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
305 310 315 320
Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335
Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
340 345 350
Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
355 360 365
Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
370 375 380
Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385 390 395 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
405 410 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
420 425 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
435 440 445
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 31
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 31
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 32
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 32
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 33
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 33
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agctcggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaagccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 34
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 34
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Ser
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Ser Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 35
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 35
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 36
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 36
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 37
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 37
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 38
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 38
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80

His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 39
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 39
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gagcgttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 40
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 40
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Ser Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 41
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 41
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180

acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaagaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag gaaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 42
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 42
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Glu Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 43
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 43
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa actgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600

gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 44
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 44
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Lys Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 45
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 45
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020

caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 46
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 46
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 47
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 47
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agctcggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
agcaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 48
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 48
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Ser
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Ser Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 49
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 49
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa actgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag gaaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 50
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 50
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Lys Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Glu Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 51
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 51
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgcaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 52
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 52
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 53
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 53
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaagaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagaaag gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcgga 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggtgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 54
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 54
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Lys Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 55
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 55
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgtgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 56
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 56
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Val Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 57
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 57
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240

catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
agcaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtt tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 58
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 58
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Ser Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Phe Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 59
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 59
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agctcggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag gaaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 60
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 60
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Ser
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Glu Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 61
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 61
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
agcaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 62
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 62
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Ser Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 63
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 63
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaagaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag gaaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 64
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 64
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Glu Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 65
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 65
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gagggttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 66
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 66
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys

420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 67
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 67
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaagaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcgga 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccaatggct ggacacgcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagcacca gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggtgaa cgtggtcgta tcgtgaagtg ggttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 68
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 68
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Thr Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 69
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 69
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcctgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagctgg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
agcaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cacctgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtt tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacagc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 70
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 7

<400> 70
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Ser Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Phe Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 71
<211> 2460
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized Thermosynechococcus elongatus sucrose synthase

<400> 71
atgcaccatc atcatcatca tggcggtagc ggcatgactt gtgttctgtt aaaagcagtt 60
gtagaaagcg acgaacgtgc cgacctgcgc cagttttcac gcattctgca actgggcgaa 120
aaacgctacc tgctgcgcaa cgacattctg gatgcgtttg cagactattg ccgcgatcaa 180
gaacgcccgg tgccaccacc gagcgaaagc cgtctgagca aactggtctt ctatacccag 240
gaaattatcg tggataacga atcactgtgt tggatcgttc gtccacgtat tgcacagcag 300
gaagtgtgcc gtttactggt cgaagacctg accattgtgc cgatgaccat cccggagctg 360
ctggatctgc gtgaccgctt ggtgaaccat tatcatccga acgaaggcga cgtgtttgag 420
attgatgtgc aaccgtttta tgactatagc ccaatcatcc gtgatgcgaa aaacatcggt 480
aagggcgtcg agttcctgaa ccgctatctt agctcgaagc tgttccagga cccgcgccaa 540
tggcaacaga acctgttcaa cttcctgcgc attcatcgct acaatggcta ccagctgctg 600
attaacgagc gcattcgtag tccgcagcat ctgagcgaac aggtcaaaca agcactggtt 660
gtgctgagcg atcgtccacc aactgaagcc tatagcgagt ttcgcttcga gctgcaaaac 720
ctgggttttg aaccaggttg gggcaatacc gttgcacgtg ttcgtgacac cctggaaatt 780
ctggaccagc tgctggatag cccggaccat caagttctgg aagcgtttgt gagccgcatc 840
ccaatgctgt tccgcattgc actgatttcg ccgcatggtt ggttcggtca ggaaggtgtt 900
ctgggtcgtc cagatacggg tggtcaggtt gtgtatatcc tggaccaggt gaagagtctg 960
gagaaacaga tgcgcgaaga ccttgaactg gccggtttag gcgttctgga agcacagccg 1020
aagatcatcg ttctgacccg cctcattcca aatgcggaag gcaccctgtg taaccaacgt 1080
ctggaaaaga tttacggcac caatgatgcg tggattctgc gcgttccatt tcgcgagttc 1140
aacccgaaag tcacgcagaa ttggattagc cgctttgaga tctggccgta cctggaaacc 1200
tttgcgattg acgccgaacg tgaactgcgt gcagaatttg gtcatgtacc ggatctgatc 1260
atcggcaatt atagcgacgg taatttggtt gcgttcctgt tagcgcgtcg cttaaaggtg 1320
acccagtgta acatcgcaca tgccctggaa aagagcaagt acctgtttag caatctgtat 1380
tggcaggatc tggaagacaa gtaccacttt agcctgcaat ttacagccga tctgattgca 1440
atgaatgcag cgaatttcat cattagcagt acctaccagg agattgttgg cactccggat 1500
tccatcggtc aatacgagag ctatcaatcc ttcaccatgc cagacctgta ccatgtggtt 1560
aatggcattg aactgttcag tccaaagttt aatgttgttc caccgggcgt taatgaacag 1620
gtgtattttc cgtattatca ttataccgaa cgcctggaag gtgatcgcca acgcctggaa 1680
gaactgcttt ttactctgga agatccgcag cagatttacg gctacctgga agcacccgaa 1740
aaacgtccgt tgttcagtat ggctcgtctg gatcgcatca agaacctgac cggtttagcc 1800
gaagcatttg gccgtagcaa ggcactgcaa gaacgttgca acctcattct ggtagcgggc 1860
aaattacgca ccgcagatag cagcgaccgt gaagaaattg cggagatcga aaaactgtac 1920
cagatcatcc accagtataa cctgcatggc aagattcgtt ggcttggtat tcgccttccg 1980
aaagccgata gcggcgaaat ctaccgcatt atcgcagatc gccagggcat ttttgtgcaa 2040
ccggcgttgt ttgaagcgtt cggcctgact attctggagg cgatgattag cggtctgccg 2100
acttttggca cccgcttcgg tggtccgctg gagatcatcc aggatggtgt caacggcttc 2160
tacattaatc cgactcatct ggaagaaatg gctgagacga ttgtgcgctt cctggaagca 2220
tgtgaccgcg atccgcagga atggcagcgc attagcaagg cgggcattga gcgtgtttat 2280
agcacctaca cgtggaagat ccattgcacc cgcctgctga gcctggccaa aatctacggc 2340
ttttggaatt ttagcagcca agaaaaccgc gaagatatga tgcgttacat ggaagcactg 2400
ttccatctgc tgtataaacc gcgtgctcag gcactgctgg ccgaacatct tcagcgttaa 2460

<210> 72
<211> 819
<212> PRT
<213> Artificial Sequence

<220>
<223> Codon optimized Thermosynechococcus elongatus sucrose synthase

<400> 72
Met His His His His His His Gly Gly Ser Gly Met Thr Cys Val Leu

1 5 10 15
Leu Lys Ala Val Val Glu Ser Asp Glu Arg Ala Asp Leu Arg Gln Phe
20 25 30
Ser Arg Ile Leu Gln Leu Gly Glu Lys Arg Tyr Leu Leu Arg Asn Asp
35 40 45
Ile Leu Asp Ala Phe Ala Asp Tyr Cys Arg Asp Gln Glu Arg Pro Val
50 55 60
Pro Pro Pro Ser Glu Ser Arg Leu Ser Lys Leu Val Phe Tyr Thr Gln
65 70 75 80
Glu Ile Ile Val Asp Asn Glu Ser Leu Cys Trp Ile Val Arg Pro Arg
85 90 95
Ile Ala Gln Gln Glu Val Cys Arg Leu Leu Val Glu Asp Leu Thr Ile
100 105 110
Val Pro Met Thr Ile Pro Glu Leu Leu Asp Leu Arg Asp Arg Leu Val
115 120 125
Asn His Tyr His Pro Asn Glu Gly Asp Val Phe Glu Ile Asp Val Gln
130 135 140
Pro Phe Tyr Asp Tyr Ser Pro Ile Ile Arg Asp Ala Lys Asn Ile Gly
145 150 155 160
Lys Gly Val Glu Phe Leu Asn Arg Tyr Leu Ser Ser Lys Leu Phe Gln
165 170 175
Asp Pro Arg Gln Trp Gln Gln Asn Leu Phe Asn Phe Leu Arg Ile His
180 185 190
Arg Tyr Asn Gly Tyr Gln Leu Leu Ile Asn Glu Arg Ile Arg Ser Pro
195 200 205
Gln His Leu Ser Glu Gln Val Lys Gln Ala Leu Val Val Leu Ser Asp
210 215 220
Arg Pro Pro Thr Glu Ala Tyr Ser Glu Phe Arg Phe Glu Leu Gln Asn
225 230 235 240
Leu Gly Phe Glu Pro Gly Trp Gly Asn Thr Val Ala Arg Val Arg Asp
245 250 255
Thr Leu Glu Ile Leu Asp Gln Leu Leu Asp Ser Pro Asp His Gln Val
260 265 270
Leu Glu Ala Phe Val Ser Arg Ile Pro Met Leu Phe Arg Ile Ala Leu
275 280 285
Ile Ser Pro His Gly Trp Phe Gly Gln Glu Gly Val Leu Gly Arg Pro
290 295 300
Asp Thr Gly Gly Gln Val Val Tyr Ile Leu Asp Gln Val Lys Ser Leu
305 310 315 320
Glu Lys Gln Met Arg Glu Asp Leu Glu Leu Ala Gly Leu Gly Val Leu
325 330 335
Glu Ala Gln Pro Lys Ile Ile Val Leu Thr Arg Leu Ile Pro Asn Ala
340 345 350
Glu Gly Thr Leu Cys Asn Gln Arg Leu Glu Lys Ile Tyr Gly Thr Asn
355 360 365
Asp Ala Trp Ile Leu Arg Val Pro Phe Arg Glu Phe Asn Pro Lys Val
370 375 380
Thr Gln Asn Trp Ile Ser Arg Phe Glu Ile Trp Pro Tyr Leu Glu Thr
385 390 395 400
Phe Ala Ile Asp Ala Glu Arg Glu Leu Arg Ala Glu Phe Gly His Val
405 410 415
Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Phe
420 425 430
Leu Leu Ala Arg Arg Leu Lys Val Thr Gln Cys Asn Ile Ala His Ala
435 440 445

Leu Glu Lys Ser Lys Tyr Leu Phe Ser Asn Leu Tyr Trp Gln Asp Leu
450 455 460
Glu Asp Lys Tyr His Phe Ser Leu Gln Phe Thr Ala Asp Leu Ile Ala
465 470 475 480
Met Asn Ala Ala Asn Phe Ile Ile Ser Ser Thr Tyr Gln Glu Ile Val
485 490 495
Gly Thr Pro Asp Ser Ile Gly Gln Tyr Glu Ser Tyr Gln Ser Phe Thr
500 505 510
Met Pro Asp Leu Tyr His Val Val Asn Gly Ile Glu Leu Phe Ser Pro
515 520 525
Lys Phe Asn Val Val Pro Pro Gly Val Asn Glu Gln Val Tyr Phe Pro
530 535 540
Tyr Tyr His Tyr Thr Glu Arg Leu Glu Gly Asp Arg Gln Arg Leu Glu
545 550 555 560
Glu Leu Leu Phe Thr Leu Glu Asp Pro Gln Gln Ile Tyr Gly Tyr Leu
565 570 575
Glu Ala Pro Glu Lys Arg Pro Leu Phe Ser Met Ala Arg Leu Asp Arg
580 585 590
Ile Lys Asn Leu Thr Gly Leu Ala Glu Ala Phe Gly Arg Ser Lys Ala
595 600 605
Leu Gln Glu Arg Cys Asn Leu Ile Leu Val Ala Gly Lys Leu Arg Thr
610 615 620
Ala Asp Ser Ser Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Leu Tyr
625 630 635 640
Gln Ile Ile His Gln Tyr Asn Leu His Gly Lys Ile Arg Trp Leu Gly
645 650 655
Ile Arg Leu Pro Lys Ala Asp Ser Gly Glu Ile Tyr Arg Ile Ile Ala
660 665 670
Asp Arg Gln Gly Ile Phe Val Gln Pro Ala Leu Phe Glu Ala Phe Gly
675 680 685
Leu Thr Ile Leu Glu Ala Met Ile Ser Gly Leu Pro Thr Phe Gly Thr
690 695 700
Arg Phe Gly Gly Pro Leu Glu Ile Ile Gln Asp Gly Val Asn Gly Phe
705 710 715 720
Tyr Ile Asn Pro Thr His Leu Glu Glu Met Ala Glu Thr Ile Val Arg
725 730 735
Phe Leu Glu Ala Cys Asp Arg Asp Pro Gln Glu Trp Gln Arg Ile Ser
740 745 750
Lys Ala Gly Ile Glu Arg Val Tyr Ser Thr Tyr Thr Trp Lys Ile His
755 760 765
Cys Thr Arg Leu Leu Ser Leu Ala Lys Ile Tyr Gly Phe Trp Asn Phe
770 775 780
Ser Ser Gln Glu Asn Arg Glu Asp Met Met Arg Tyr Met Glu Ala Leu
785 790 795 800
Phe His Leu Leu Tyr Lys Pro Arg Ala Gln Ala Leu Leu Ala Glu His
805 810 815
Leu Gln Arg

<210> 73
<211> 2415
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized Acidithiobacillus caldus sucrose synthase

<400> 73
atgcaccatc atcatcatca tggcggtagc ggcatgattg aagcactgcg ccaacagctg 60
ctggatgatc cacgttcatg gtacgcattc ctgcgtcatt tagtcgcatc tcagcgtgac 120
tcatggttat atacggattt acagcgcgcg tgcgcggatt ttcgcgaaca gctgccggaa 180
ggctatgcag aaggtattgg tccgctcgaa gattttgtgg cacataccca ggaagtgatc 240
ttccgtgatc cgtggatggt ttttgcgtgg cgtccacgtc caggtcgttg gatttatgtg 300
cgcattcatc gtgaacagct ggccctggag gagctgagca ctgatgccta tctgcaagcc 360
aaagaaggca tcgttggctt aggtgcagaa ggtgaagcag ttctgacggt ggatttccgc 420
gattttcgtc cggttagccg tcgtttacgc gacgagagca ccattggtga tggtcttacc 480
catctgaatc gtcgtttagc aggtcgcatc tttagcgatt tagcagcagg tcgtagtcag 540
atcctggaat ttctgagcct gcatcgtctg gatggtcaga atctgatgct gagcaacggc 600
aataccgatt ttgactcttt acgtcaaacc gtacagtatc tgggcacctt accacgtgaa 660
actccgtggg cagagattcg tgaagacatg cgtcgtcgtg gttttgcacc aggttggggc 720
aacaccgcgg gccgtgttcg cgaaaccatg cgtctgctga tggatctgct tgactctccg 780
agcccagctg ccctggagag cttcctggat cgcatcccga tgattagccg catcctgatc 840
gtgagcattc acggatggtt tgcgcaggac aaggttctgg gtcgtccgga cactggtggt 900
caggtcgtgt atattctgga tcaggcccgt gcactggaac gcgaaatgcg taaccgcctg 960
cgccaacagg gtgttgatgt ggagccgcgc attttgattg cgacccgttt aatcccggaa 1020
agtgatggca cgacttgtga ccagcgtctg gagcctgtcg taggtgccga gaatgtgcag 1080
attctgcgcg ttccgtttcg ctatccagat ggtcgtattc acccgcattg gatctcacgc 1140
ttcaagattt ggccgtggct tgaacgctat gcacaggatc tggaacgcga agttctggcc 1200
gaattaggta gtcgtccaga tctgatcatc ggcaactata gcgacggtaa tctggttgca 1260
accctgctgt cagaacgctt aggtgttacg cagtgcaaca ttgcacatgc cctggagaaa 1320
agcaagtacc tgtactccga tctgcattgg cgcgatcatg aacaggacca tcactttgca 1380
tgtcagttta ccgcggatct gatcgcgatg aatgcagcag acatcatcgt gacgagcaca 1440
taccaggaaa ttgcaggtaa tgaccgcgag atcggtcaat atgaaggtca ccaggactat 1500
actttaccgg gcttgtatcg tgtcgagaat ggtattgacg tgttcgatag caagtttaac 1560
attgtgagtc cgggcgcaga tccacgcttt tattttagct atgcacgtac tgaagaacgc 1620
ccatcgttcc tggagccaga aatcgaaagt ctgctgtttg gccgcgaacc aggtgcagat 1680
cgtcgtggtg ttctcgaaga tcgccagaaa ccgctgctgc tgtcgatggc ccgtatggat 1740
cgcatcaaga acctgagcgg tctggccgaa ctgtatggtc gtagttctcg cttacgtggt 1800
ctggccaatt tggtgatcat cggtggtcat gttgatgtgg gcaatagtcg cgatgcagaa 1860
gaacgcgaag aaatccgtcg tatgcacgag atcatggacc attaccagct ggatggtcag 1920
ctgcgttggg tgggagcact gctggataaa accgtggcgg gcgaattgta tcgtgtagtg 1980
gcggatggtc gtggcgtttt tgtgcaacca gccctgtttg aggcgttcgg cctgaccgtg 2040
attgaggcaa tgagcagtgg cctgccagtg tttgcgaccc gcttcggtgg tccgctggaa 2100
atcatcgaag acggcgttag cggcttccat attgatccca acgaccatga agcgaccgca 2160
gaacgtctgg ccgacttcct ggaagcagcg cgtgaacgtc cgaaatattg gcttgaaatt 2220
agcgatgcgg ctcttgcgcg cgtcgcggaa cgttacacgt gggagcgcta tgcggaacgc 2280
ttgatgacca tcgcgcgtat cttcggcttt tggcgcttcg ttctggatcg cgaatcacag 2340
gtcatggaac gctatctgca aatgttccgc cacctgcaat ggcgcccgct ggctcatgcc 2400
gtaccgatgg agtaa 2415

<210> 74
<211> 804
<212> PRT
<213> Artificial Sequence

<220>
<223> Codon optimized Acidithiobacillus caldus sucrose synthase

<400> 74
Met His His His His His His Gly Gly Ser Gly Met Ile Glu Ala Leu
1 5 10 15
Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp Tyr Ala Phe Leu Arg
20 25 30
His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu Tyr Thr Asp Leu Gln
35 40 45
Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro Glu Gly Tyr Ala Glu
50 55 60
Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His Thr Gln Glu Val Ile
65 70 75 80
Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg Pro Arg Pro Gly Arg
85 90 95
Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu Ala Leu Glu Glu Leu
100 105 110
Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly Ile Val Gly Leu Gly
115 120 125
Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe Arg Asp Phe Arg Pro
130 135 140
Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile Gly Asp Gly Leu Thr
145 150 155 160
His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe Ser Asp Leu Ala Ala
165 170 175
Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu His Arg Leu Asp Gly
180 185 190
Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp Phe Asp Ser Leu Arg
195 200 205
Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg Glu Thr Pro Trp Ala
210 215 220
Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe Ala Pro Gly Trp Gly
225 230 235 240
Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg Leu Leu Met Asp Leu
245 250 255
Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser Phe Leu Asp Arg Ile
260 265 270
Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile His Gly Trp Phe Ala
275 280 285
Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly Gly Gln Val Val Tyr
290 295 300
Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu Met Arg Asn Arg Leu
305 310 315 320
Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile Leu Ile Ala Thr Arg
325 330 335
Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp Gln Arg Leu Glu Pro
340 345 350
Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg Val Pro Phe Arg Tyr
355 360 365
Pro Asp Gly Arg Ile His Pro His Trp Ile Ser Arg Phe Lys Ile Trp
370 375 380
Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu Arg Glu Val Leu Ala
385 390 395 400
Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly
405 410 415
Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu Gly Val Thr Gln Cys
420 425 430

Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr Leu Tyr Ser Asp Leu
435 440 445
His Trp Arg Asp His Glu Gln Asp His His Phe Ala Cys Gln Phe Thr
450 455 460
Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile Ile Val Thr Ser Thr
465 470 475 480
Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile Gly Gln Tyr Glu Gly
485 490 495
His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg Val Glu Asn Gly Ile
500 505 510
Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Pro
515 520 525
Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu Arg Pro Ser Phe Leu
530 535 540
Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg Glu Pro Gly Ala Asp
545 550 555 560
Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro Leu Leu Leu Ser Met
565 570 575
Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly Leu Ala Glu Leu Tyr
580 585 590
Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn Leu Val Ile Ile Gly
595 600 605
Gly His Val Asp Val Gly Asn Ser Arg Asp Ala Glu Glu Arg Glu Glu
610 615 620
Ile Arg Arg Met His Glu Ile Met Asp His Tyr Gln Leu Asp Gly Gln
625 630 635 640
Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr Val Ala Gly Glu Leu
645 650 655
Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe Val Gln Pro Ala Leu
660 665 670
Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met Ser Ser Gly Leu
675 680 685
Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu Glu Ile Ile Glu Asp
690 695 700
Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp His Glu Ala Thr Ala
705 710 715 720
Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg Glu Arg Pro Lys Tyr
725 730 735
Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg Val Ala Glu Arg Tyr
740 745 750
Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr Ile Ala Arg Ile Phe
755 760 765
Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser Gln Val Met Glu Arg
770 775 780
Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg Pro Leu Ala His Ala
785 790 795 800
Val Pro Met Glu

<210> 75
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 75
atgccgcagg acgagcgtat tagcaacctg ccgacccatg gtccgctggc gggtatgcgt 60
atcccgatca ttaacgagca cggcgcggat gaactgcgtc gtgagctgga actgctgatg 120
ctggcgagcg aggaagacga ggaagttagc tgcctgatta ccgatgcgct gtggtacttc 180
gcgcaaagcg tggcggacag cctgaacctg cgtcgtctgg ttctgatgac cagcagcctg 240
tttaacttcc acgcgcacgt gagcctgccg cagtttgacg agcttggcta cctggatccg 300
gacgataaaa cccgtctgga ggaacaagcg agcggtttcc cgatgctgaa ggttaaagat 360
atcaagagcg cgtatagcaa ctggcagatc ctgaaagaaa ttctgggcaa gatgatcaag 420
cagacccgtg cgagcagcgg tgtgatttgg aacagcttta aagagctgga ggaaagcgag 480
ctggaaaccg ttatccgtga aattccggcg ccgagcttcc tgattccgct gccgaagcac 540
ctgaccgcga gcagcagcag cctgctggac cacgatcgta ccgtgttcca gtggctggac 600
cagcaaccgc cgagcagcgt gctgtacgtt agctttggca gccagagcga ggtggacgaa 660
aaggatttcc tggagattgc gcgtggtctg gttgacagca aacaaagctt tctgtggcgc 720
gttcgtccgg gcttcgtgaa gggtagcgag tgggttgagc cgctgccgga tggttttctg 780
ggcgaacgtg gtcgtatcgt gaagtctgtt ccgcaacaag aagtgctggc gcacggcgcg 840
attggtgcgt tctggaccca cagcggttgg aacggcaccc tggagagcgt gtgcgaaggc 900
gttccgatga tctttagcga cttcggtctg gatcagccgc tgaacgcgcg ttacatgagc 960
gatgttctga aagtgggcgt ttatctggag aacggctggg agcgtggtga aatcgcgaac 1020
gcgattcgtc gtgtgatggt tgacgaggaa ggtgagtaca tccgtcagaa cgcgcgtgtt 1080
ctgaagcaaa aagcggatgt tagcctgatg aagggtggca gcagctacga gagcctggaa 1140
agcctggtta gctatattag cagcctcgag catcaccatc accatcacgg tggcagcggt 1200
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 1260
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 1320
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 1380
acctttcgtt tcatcttgga caacgattaa 1410

<210> 76
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 76
Met Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu
1 5 10 15
Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu
20 25 30
Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu
35 40 45
Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val
50 55 60
Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu
65 70 75 80
Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly
85 90 95
Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly
100 105 110
Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp
115 120 125

Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala
130 135 140
Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu
145 150 155 160
Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro
165 170 175
Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp
180 185 190
Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu
195 200 205
Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu
210 215 220
Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg
225 230 235 240
Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro
245 250 255
Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln
260 265 270
Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser
275 280 285
Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile
290 295 300
Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser
305 310 315 320
Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly
325 330 335
Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu
340 345 350
Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser
355 360 365
Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser
370 375 380
Tyr Ile Ser Ser Leu Glu His His His His His His Gly Gly Ser Gly
385 390 395 400
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
405 410 415
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
420 425 430
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
435 440 445
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
450 455 460
Ile Leu Asp Asn Asp
465

<210> 77
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 77

atgcaggacg agcgtattag caacctgccg acccatggtc cgctggcggg tatgcgtatc 60
ccgatcatta acgagcacgg cgcggatgaa ctgcgtcgtg agctggaact gctgatgctg 120
gcgagcgagg aagacgagga agttagctgc ctgattaccg atgcgctgtg gtacttcgcg 180
caaagcgtgg cggacagcct gaacctgcgt cgtctggttc tgatgaccag cagcctgttt 240
aacttccacg cgcacgtgag cctgccgcag tttgacgagc ttggctacct ggatccggac 300
gataaaaccc gtctggagga acaagcgagc ggtttcccga tgctgaaggt taaagatatc 360
aagagcgcgt atagcaactg gcagatcctg aaagaaattc tgggcaagat gatcaagcag 420
acccgtgcga gcagcggtgt gatttggaac agctttaaag agctggagga aagcgagctg 480
gaaaccgtta tccgtgaaat tccggcgccg agcttcctga ttccgctgcc gaagcacctg 540
accgcgagca gcagcagcct gctggaccac gatcgtaccg tgttccagtg gctggaccag 600
caaccgccga gcagcgtgct gtacgttagc tttggcagcc agagcgaggt ggacgaaaag 660
gatttcctgg agattgcgcg tggtctggtt gacagcaaac aaagctttct gtggcgcgtt 720
cgtccgggct tcgtgaaggg tagcgagtgg gttgagccgc tgccggatgg ttttctgggc 780
gaacgtggtc gtatcgtgaa gtctgttccg caacaagaag tgctggcgca cggcgcgatt 840
ggtgcgttct ggacccacag cggttggaac ggcaccctgg agagcgtgtg cgaaggcgtt 900
ccgatgatct ttagcgactt cggtctggat cagccgctga acgcgcgtta catgagcgat 960
gttctgaaag tgggcgttta tctggagaac ggctgggagc gtggtgaaat cgcgaacgcg 1020
attcgtcgtg tgatggttga cgaggaaggt gagtacatcc gtcagaacgc gcgtgttctg 1080
aagcaaaaag cggatgttag cctgatgaag ggtggcagca gctacgagag cctggaaagc 1140
ctggttagct atattagcag cctcgagcat caccatcacc atcacggtgg cagcggtatg 1200
gagaacaaaa ccgaaaccac cgtgcgtcgt cgtcgtatca ttctgtttcc ggttccgttc 1260
cagggccaca tcaacccgat tctgcaactg gcgaacgtgc tgtacagcaa gggttttagc 1320
atcaccattt ttcacaccaa cttcaacaag ccgaaaacca gcaactatcc gcacttcacc 1380
tttcgtttca tcttggacaa cgatccgtaa 1410

<210> 78
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 78
Met Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala
1 5 10 15
Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg
20 25 30
Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val
35 40 45
Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala
50 55 60
Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe
65 70 75 80
Asn Phe His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr
85 90 95
Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe
100 105 110
Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln
115 120 125
Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser
130 135 140
Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu
145 150 155 160

Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu
165 170 175
Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg
180 185 190
Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr
195 200 205
Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu
210 215 220
Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val
225 230 235 240
Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp
245 250 255
Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln
260 265 270
Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly
275 280 285
Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe
290 295 300
Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp
305 310 315 320
Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu
325 330 335
Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr
340 345 350
Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu
355 360 365
Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr
370 375 380
Ile Ser Ser Leu Glu His His His His His His Gly Gly Ser Gly Met
385 390 395 400
Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe
405 410 415
Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn
420 425 430
Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe
435 440 445
Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile
450 455 460
Leu Asp Asn Asp Pro
465

<210> 79
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 79
atggacgagc gtattagcaa cctgccgacc catggtccgc tggcgggtat gcgtatcccg 60
atcattaacg agcacggcgc ggatgaactg cgtcgtgagc tggaactgct gatgctggcg 120
agcgaggaag acgaggaagt tagctgcctg attaccgatg cgctgtggta cttcgcgcaa 180
agcgtggcgg acagcctgaa cctgcgtcgt ctggttctga tgaccagcag cctgtttaac 240

ttccacgcgc acgtgagcct gccgcagttt gacgagcttg gctacctgga tccggacgat 300
aaaacccgtc tggaggaaca agcgagcggt ttcccgatgc tgaaggttaa agatatcaag 360
agcgcgtata gcaactggca gatcctgaaa gaaattctgg gcaagatgat caagcagacc 420
cgtgcgagca gcggtgtgat ttggaacagc tttaaagagc tggaggaaag cgagctggaa 480
accgttatcc gtgaaattcc ggcgccgagc ttcctgattc cgctgccgaa gcacctgacc 540
gcgagcagca gcagcctgct ggaccacgat cgtaccgtgt tccagtggct ggaccagcaa 600
ccgccgagca gcgtgctgta cgttagcttt ggcagccaga gcgaggtgga cgaaaaggat 660
ttcctggaga ttgcgcgtgg tctggttgac agcaaacaaa gctttctgtg gcgcgttcgt 720
ccgggcttcg tgaagggtag cgagtgggtt gagccgctgc cggatggttt tctgggcgaa 780
cgtggtcgta tcgtgaagtc tgttccgcaa caagaagtgc tggcgcacgg cgcgattggt 840
gcgttctgga cccacagcgg ttggaacggc accctggaga gcgtgtgcga aggcgttccg 900
atgatcttta gcgacttcgg tctggatcag ccgctgaacg cgcgttacat gagcgatgtt 960
ctgaaagtgg gcgtttatct ggagaacggc tgggagcgtg gtgaaatcgc gaacgcgatt 1020
cgtcgtgtga tggttgacga ggaaggtgag tacatccgtc agaacgcgcg tgttctgaag 1080
caaaaagcgg atgttagcct gatgaagggt ggcagcagct acgagagcct ggaaagcctg 1140
gttagctata ttagcagcct cgagcatcac catcaccatc acggtggcag cggtatggag 1200
aacaaaaccg aaaccaccgt gcgtcgtcgt cgtatcattc tgtttccggt tccgttccag 1260
ggccacatca acccgattct gcaactggcg aacgtgctgt acagcaaggg ttttagcatc 1320
accatttttc acaccaactt caacaagccg aaaaccagca actatccgca cttcaccttt 1380
cgtttcatct tggacaacga tccgcagtaa 1410

<210> 80
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 80
Met Asp Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala Gly
1 5 10 15
Met Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg Arg
20 25 30
Glu Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val Ser
35 40 45
Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp
50 55 60
Ser Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe Asn
65 70 75 80
Phe His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu
85 90 95
Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro
100 105 110
Met Leu Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile
115 120 125
Leu Lys Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser
130 135 140
Gly Val Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu
145 150 155 160
Thr Val Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro
165 170 175
Lys His Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr
180 185 190

Val Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val
195 200 205
Ser Phe Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile
210 215 220
Ala Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg
225 230 235 240
Pro Gly Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly
245 250 255
Phe Leu Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu
260 265 270
Val Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp
275 280 285
Asn Gly Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser
290 295 300
Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val
305 310 315 320
Leu Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile
325 330 335
Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr Ile
340 345 350
Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu Met
355 360 365
Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile
370 375 380
Ser Ser Leu Glu His His His His His His Gly Gly Ser Gly Met Glu
385 390 395 400
Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe Pro
405 410 415
Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val
420 425 430
Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn
435 440 445
Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu
450 455 460
Asp Asn Asp Pro Gln
465

<210> 81
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 81
atggagcgta ttagcaacct gccgacccat ggtccgctgg cgggtatgcg tatcccgatc 60
attaacgagc acggcgcgga tgaactgcgt cgtgagctgg aactgctgat gctggcgagc 120
gaggaagacg aggaagttag ctgcctgatt accgatgcgc tgtggtactt cgcgcaaagc 180
gtggcggaca gcctgaacct gcgtcgtctg gttctgatga ccagcagcct gtttaacttc 240
cacgcgcacg tgagcctgcc gcagtttgac gagcttggct acctggatcc ggacgataaa 300
acccgtctgg aggaacaagc gagcggtttc ccgatgctga aggttaaaga tatcaagagc 360
gcgtatagca actggcagat cctgaaagaa attctgggca agatgatcaa gcagacccgt 420
gcgagcagcg gtgtgatttg gaacagcttt aaagagctgg aggaaagcga gctggaaacc 480

gttatccgtg aaattccggc gccgagcttc ctgattccgc tgccgaagca cctgaccgcg 540
agcagcagca gcctgctgga ccacgatcgt accgtgttcc agtggctgga ccagcaaccg 600
ccgagcagcg tgctgtacgt tagctttggc agccagagcg aggtggacga aaaggatttc 660
ctggagattg cgcgtggtct ggttgacagc aaacaaagct ttctgtggcg cgttcgtccg 720
ggcttcgtga agggtagcga gtgggttgag ccgctgccgg atggttttct gggcgaacgt 780
ggtcgtatcg tgaagtctgt tccgcaacaa gaagtgctgg cgcacggcgc gattggtgcg 840
ttctggaccc acagcggttg gaacggcacc ctggagagcg tgtgcgaagg cgttccgatg 900
atctttagcg acttcggtct ggatcagccg ctgaacgcgc gttacatgag cgatgttctg 960
aaagtgggcg tttatctgga gaacggctgg gagcgtggtg aaatcgcgaa cgcgattcgt 1020
cgtgtgatgg ttgacgagga aggtgagtac atccgtcaga acgcgcgtgt tctgaagcaa 1080
aaagcggatg ttagcctgat gaagggtggc agcagctacg agagcctgga aagcctggtt 1140
agctatatta gcagcctcga gcatcaccat caccatcacg gtggcagcgg tatggagaac 1200
aaaaccgaaa ccaccgtgcg tcgtcgtcgt atcattctgt ttccggttcc gttccagggc 1260
cacatcaacc cgattctgca actggcgaac gtgctgtaca gcaagggttt tagcatcacc 1320
atttttcaca ccaacttcaa caagccgaaa accagcaact atccgcactt caccttcgt 1380
ttcatcttgg acaacgatcc gcaggactaa 1410

<210> 82
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 82
Met Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala Gly Met
1 5 10 15
Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg Arg Glu
20 25 30
Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val Ser Cys
35 40 45
Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser
50 55 60
Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe Asn Phe
65 70 75 80
His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp
85 90 95
Pro Asp Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met
100 105 110
Leu Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu
115 120 125
Lys Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly
130 135 140
Val Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr
145 150 155 160
Val Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys
165 170 175
His Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val
180 185 190
Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser
195 200 205
Phe Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala
210 215 220

Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro
225 230 235 240
Gly Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe
245 250 255
Leu Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val
260 265 270
Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn
275 280 285
Gly Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp
290 295 300
Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu
305 310 315 320
Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile Ala
325 330 335
Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr Ile Arg
340 345 350
Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu Met Lys
355 360 365
Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile Ser
370 375 380
Ser Leu Glu His His His His His His Gly Gly Ser Gly Met Glu Asn
385 390 395 400
Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe Pro Val
405 410 415
Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu
420 425 430
Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys
435 440 445
Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp
450 455 460
Asn Asp Pro Gln Asp
465

<210> 83
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 83
atgcgtatta gcaacctgcc gacccatggt ccgctggcgg gtatgcgtat cccgatcatt 60
aacgagcacg gcgcggatga actgcgtcgt gagctggaac tgctgatgct ggcgagcgag 120
gaagacgagg aagttagctg cctgattacc gatgcgctgt ggtacttcgc gcaaagcgtg 180
gcggacagcc tgaacctgcg tcgtctggtt ctgatgacca gcagcctgtt taacttccac 240
gcgcacgtga gcctgccgca gtttgacgag cttggctacc tggatccgga cgataaaacc 300
cgtctggagg aacaagcgag cggtttcccg atgctgaagg ttaaagatat caagagcgcg 360
tatagcaact ggcagatcct gaaagaaatt ctgggcaaga tgatcaagca gacccgtgcg 420
agcagcggtg tgatttggaa cagctttaaa gagctggagg aaagcgagct ggaaaccgtt 480
atccgtgaaa ttccggcgcc gagcttcctg attccgctgc cgaagcacct gaccgcgagc 540
agcagcagcc tgctggacca cgatcgtacc gtgttccagt ggctggacca gcaaccgccg 600
agcagcgtgc tgtacgttag ctttggcagc cagagcgagg tggacgaaaa ggatttcctg 660
gagattgcgc gtggtctggt tgacagcaaa caaagctttc tgtggcgcgt tcgtccgggc 720

ttcgtgaagg gtagcgagtg ggttgagccg ctgccggatg gttttctggg cgaacgtggt 780
cgtatcgtga agtctgttcc gcaacaagaa gtgctggcgc acggcgcgat tggtgcgttc 840
tggacccaca gcggttggaa cggcaccctg gagagcgtgt gcgaaggcgt tccgatgatc 900
tttagcgact tcggtctgga tcagccgctg aacgcgcgtt acatgagcga tgttctgaaa 960
gtgggcgttt atctggagaa cggctgggag cgtggtgaaa tcgcgaacgc gattcgtcgt 1020
gtgatggttg acgaggaagg tgagtacatc cgtcagaacg cgcgtgttct gaagcaaaaa 1080
gcggatgtta gcctgatgaa gggtggcagc agctacgaga gcctggaaag cctggttagc 1140
tatattagca gcctcgagca tcaccatcac catcacggtg gcagcggtat ggagaacaaa 1200
accgaaacca ccgtgcgtcg tcgtcgtatc attctgtttc cggttccgtt ccagggccac 1260
atcaacccga ttctgcaact ggcgaacgtg ctgtacagca agggttttag catcaccatt 1320
tttcacacca acttcaacaa gccgaaaacc agcaactatc cgcacttcac ctttcgtttc 1380
atcttggaca acgatccgca ggacgagtaa 1410

<210> 84
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 84
Met Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg
1 5 10 15
Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu
20 25 30
Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu
35 40 45
Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu
50 55 60
Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe Asn Phe His
65 70 75 80
Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro
85 90 95
Asp Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu
100 105 110
Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys
115 120 125
Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val
130 135 140
Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val
145 150 155 160
Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His
165 170 175
Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe
180 185 190
Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe
195 200 205
Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg
210 215 220
Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly
225 230 235 240
Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu
245 250 255

Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu
260 265 270
Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly
275 280 285
Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp Phe
290 295 300
Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu Lys
305 310 315 320
Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn
325 330 335
Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln
340 345 350
Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu Met Lys Gly
355 360 365
Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser
370 375 380
Leu Glu His His His His His His Gly Gly Ser Gly Met Glu Asn Lys
385 390 395 400
Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe Pro Val Pro
405 410 415
Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu Tyr
420 425 430
Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys Pro
435 440 445
Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp Asn
450 455 460
Asp Pro Gln Asp Glu
465

<210> 85
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 85
atgattagca acctgccgac ccatggtccg ctggcgggta tgcgtatccc gatcattaac 60
gagcacggcg cggatgaact gcgtcgtgag ctggaactgc tgatgctggc gagcgaggaa 120
gacgaggaag ttagctgcct gattaccgat gcgctgtggt acttcgcgca aagcgtggcg 180
gacagcctga acctgcgtcg tctggttctg atgaccagca gcctgtttaa cttccacgcg 240
cacgtgagcc tgccgcagtt tgacgagctt ggctacctgg atccggacga taaaacccgt 300
ctggaggaac aagcgagcgg tttcccgatg ctgaaggtta aagatatcaa gagcgcgtat 360
agcaactggc agatcctgaa agaaattctg ggcaagatga tcaagcagac ccgtgcgagc 420
agcggtgtga tttggaacag ctttaaagag ctggaggaaa gcgagctgga aaccgttatc 480
cgtgaaattc cggcgccgag cttcctgatt ccgctgccga agcacctgac cgcgagcagc 540
agcagcctgc tggaccacga tcgtaccgtg ttccagtggc tggaccagca accgccgagc 600
agcgtgctgt acgttagctt tggcagccag agcgaggtgg acgaaaagga tttcctggag 660
attgcgcgtg gtctggttga cagcaaacaa agctttctgt ggcgcgttcg tccgggcttc 720
gtgaagggta gcgagtgggt tgagccgctg ccggatggtt ttctgggcga acgtggtcgt 780
atcgtgaagt ctgttccgca acaagaagtg ctggcgcacg gcgcgattgg tgcgttctgg 840
acccacagcg gttggaacgg caccctggag agcgtgtgcg aaggcgttcc gatgatcttt 900
agcgacttcg gtctggatca gccgctgaac gcgcgttaca tgagcgatgt tctgaaagtg 960

ggcgtttatc tggagaacgg ctgggagcgt ggtgaaatcg cgaacgcgat tcgtcgtgtg 1020
atggttgacg aggaaggtga gtacatccgt cagaacgcgc gtgttctgaa gcaaaaagcg 1080
gatgttagcc tgatgaaggg tggcagcagc tacgagagcc tggaaagcct ggttagctat 1140
attagcagcc tcgagcatca ccatcaccat cacggtggca gcggtatgga gaacaaaacc 1200
gaaaccaccg tgcgtcgtcg tcgtatcatt ctgtttccgg ttccgttcca gggccacatc 1260
aacccgattc tgcaactggc gaacgtgctg tacagcaagg gttttagcat caccattttt 1320
cacaccaact tcaacaagcc gaaaaccagc aactatccgc acttcacctt tcgtttcatc 1380
ttggacaacg atccgcagga cgagcgttaa 1410

<210> 86
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 86
Met Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg Ile
1 5 10 15
Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu
20 25 30
Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu Ile
35 40 45
Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu Asn
50 55 60
Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe Asn Phe His Ala
65 70 75 80
His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp
85 90 95
Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys
100 105 110
Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu
115 120 125
Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile
130 135 140
Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile
145 150 155 160
Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu
165 170 175
Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe Gln
180 185 190
Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe Gly
195 200 205
Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly
210 215 220
Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly Phe
225 230 235 240
Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu Gly
245 250 255
Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu Ala
260 265 270
His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly Thr
275 280 285

Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly
290 295 300
Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val
305 310 315 320
Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala
325 330 335
Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn
340 345 350
Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu Met Lys Gly Gly
355 360 365
Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
370 375 380
Glu His His His His His His Gly Gly Ser Gly Met Glu Asn Lys Thr
385 390 395 400
Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe Pro Val Pro Phe
405 410 415
Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu Tyr Ser
420 425 430
Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys Pro Lys
435 440 445
Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp Asn Asp
450 455 460
Pro Gln Asp Glu Arg
465

<210> 87
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 87
atggacgata aaacccgtct ggaggaacaa gcgagcggtt tcccgatgct gaaggttaaa 60
gatatcaaga gcgcgtatag caactggcag atcctgaaag aaattctggg caagatgatc 120
aagcagaccc gtgcgagcag cggtgtgatt tggaacagct ttaaagagct ggaggaaagc 180
gagctggaaa ccgttatccg tgaaattccg gcgccgagct tcctgattcc gctgccgaag 240
cacctgaccg cgagcagcag cagcctgctg gaccacgatc gtaccgtgtt ccagtggctg 300
gaccagcaac cgccgagcag cgtgctgtac gttagctttg gcagccagag cgaggtggac 360
gaaaaggatt tcctggagat tgcgcgtggt ctggttgaca gcaaacaaag ctttctgtgg 420
cgcgttcgtc cgggcttcgt gaagggtagc gagtgggttg agccgctgcc ggatggtttt 480
ctgggcgaac gtggtcgtat cgtgaagtct gttccgcaac aagaagtgct ggcgcacggc 540
gcgattggtg cgttctggac ccacagcggt tggaacggca ccctggagag cgtgtgcgaa 600
ggcgttccga tgatctttag cgacttcggt ctggatcagc cgctgaacgc gcgttacatg 660
agcgatgttc tgaaagtggg cgtttatctg gagaacggct gggagcgtgg tgaaatcgcg 720
aacgcgattc gtcgtgtgat ggttgacgag gaaggtgagt acatccgtca gaacgcgcgt 780
gttctgaagc aaaaagcgga tgttagcctg atgaagggtg gcagcagcta cgagagcctg 840
gaaagcctgg ttagctatat tagcagcctc gagcatcacc atcaccatca cggtggcagc 900
ggtatggaga acaaaaccga aaccaccgtg cgtcgtcgtc gtatcattct gtttccggtt 960
ccgttccagg gccacatcaa cccgattctg caactggcga acgtgctgta cagcaagggt 1020
tttagcatca ccatttttca caccaacttc aacaagccga aaaccagcaa ctatccgcac 1080
ttcacctttc gtttcatctt ggacaacgat ccgcaggacg agcgtattag caacctgccg 1140
acccatggtc cgctggcggg tatgcgtatc ccgatcatta acgagcacgg cgcggatgaa 1200

ctgcgtcgtg agctggaact gctgatgctg gcgagcgagg aagacgagga agttagctgc 1260
ctgattaccg atgcgctgtg gtacttcgcg caaagcgtgg cggacagcct gaacctgcgt 1320
cgtctggttc tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 1380
tttgacgagc ttggctacct ggatccgtaa 1410

<210> 88
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 88
Met Asp Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met
1 5 10 15
Leu Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu
20 25 30
Lys Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly
35 40 45
Val Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr
50 55 60
Val Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys
65 70 75 80
His Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val
85 90 95
Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser
100 105 110
Phe Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala
115 120 125
Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro
130 135 140
Gly Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe
145 150 155 160
Leu Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val
165 170 175
Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn
180 185 190
Gly Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp
195 200 205
Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu
210 215 220
Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile Ala
225 230 235 240
Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr Ile Arg
245 250 255
Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu Met Lys
260 265 270
Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile Ser
275 280 285
Ser Leu Glu His His His His His His Gly Gly Ser Gly Met Glu Asn
290 295 300
Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe Pro Val
305 310 315 320

Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu
325 330 335
Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys
340 345 350
Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp
355 360 365
Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro
370 375 380
Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu
385 390 395 400
Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu
405 410 415
Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser
420 425 430
Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser
435 440 445
Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu
450 455 460
Gly Tyr Leu Asp Pro
465

<210> 89
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 89
atggataaaa cccgtctgga ggaacaagcg agcggtttcc cgatgctgaa ggttaaagat 60
atcaagagcg cgtatagcaa ctggcagatc ctgaaagaaa ttctgggcaa gatgatcaag 120
cagacccgtg cgagcagcgg tgtgatttgg aacagcttta aagagctgga ggaaagcgag 180
ctggaaaccg ttatccgtga aattccggcg ccgagcttcc tgattccgct gccgaagcac 240
ctgaccgcga gcagcagcag cctgctggac cacgatcgta ccgtgttcca gtggctggac 300
cagcaaccgc cgagcagcgt gctgtacgtt agctttggca gccagagcga ggtggacgaa 360
aaggatttcc tggagattgc gcgtggtctg gttgacagca aacaaagctt tctgtggcgc 420
gttcgtccgg gcttcgtgaa gggtagcgag tgggttgagc cgctgccgga tggttttctg 480
ggcgaacgtg gtcgtatcgt gaagtctgtt ccgcaacaag aagtgctggc gcacggcgcg 540
attggtgcgt tctggaccca cagcggttgg aacggcaccc tggagagcgt gtgcgaaggc 600
gttccgatga tctttagcga cttcggtctg gatcagccgc tgaacgcgcg ttacatgagc 660
gatgttctga aagtgggcgt ttatctggag aacggctggg agcgtggtga aatcgcgaac 720
gcgattcgtc gtgtgatggt tgacgaggaa ggtgagtaca tccgtcagaa cgcgcgtgtt 780
ctgaagcaaa aagcggatgt tagcctgatg aagggtggca gcagctacga gagcctggaa 840
agcctggtta gctatattag cagcctcgag catcaccatc accatcacgg tggcagcggt 900
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 960
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 1020
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 1080
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 1140
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 1200
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 1260
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 1320
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 1380
gacgagcttg gctacctgga tccggactaa 1410

<210> 90
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 90
Met Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu
1 5 10 15
Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys
20 25 30
Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val
35 40 45
Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val
50 55 60
Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His
65 70 75 80
Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe
85 90 95
Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe
100 105 110
Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg
115 120 125
Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly
130 135 140
Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu
145 150 155 160
Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu
165 170 175
Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly
180 185 190
Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp Phe
195 200 205
Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu Lys
210 215 220
Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn
225 230 235 240
Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln
245 250 255
Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu Met Lys Gly
260 265 270
Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser
275 280 285
Leu Glu His His His His His His Gly Gly Ser Gly Met Glu Asn Lys
290 295 300
Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe Pro Val Pro
305 310 315 320
Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu Tyr
325 330 335
Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys Pro
340 345 350

Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp Asn
355 360 365
Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu
370 375 380
Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu
385 390 395 400
Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu
405 410 415
Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val
420 425 430
Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu
435 440 445
Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly
450 455 460
Tyr Leu Asp Pro Asp
465

<210> 91
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 91
atgaaaaccc gtctggagga acaagcgagc ggtttcccga tgctgaaggt taaagatatc 60
aagagcgcgt atagcaactg gcagatcctg aaagaaattc tgggcaagat gatcaagcag 120
acccgtgcga gcagcggtgt gatttggaac agctttaaag agctggagga aagcgagctg 180
gaaaccgtta tccgtgaaat tccggcgccg agcttcctga ttccgctgcc gaagcacctg 240
accgcgagca gcagcagcct gctggaccac gatcgtaccg tgttccagtg gctggaccag 300
caaccgccga gcagcgtgct gtacgttagc tttggcagcc agagcgaggt ggacgaaaag 360
gatttcctgg agattgcgcg tggtctggtt gacagcaaac aaagctttct gtggcgcgtt 420
cgtccgggct tcgtgaaggg tagcgagtgg gttgagccgc tgccggatgg ttttctgggc 480
gaacgtggtc gtatcgtgaa gtctgttccg caacaagaag tgctggcgca cggcgcgatt 540
ggtgcgttct ggacccacag cggttggaac ggcaccctgg agagcgtgtg cgaaggcgtt 600
ccgatgatct ttagcgactt cggtctggat cagccgctga acgcgcgtta catgagcgat 660
gttctgaaag tgggcgttta tctggagaac ggctgggagc gtggtgaaat cgcgaacgcg 720
attcgtcgtg tgatggttga cgaggaaggt gagtacatcc gtcagaacgc gcgtgttctg 780
aagcaaaaag cggatgttag cctgatgaag ggtggcagca gctacgagag cctggaaagc 840
ctggttagct atattagcag cctcgagcat caccatcacc atcacggtgg cagcggtatg 900
gagaacaaaa ccgaaaccac cgtgcgtcgt cgtcgtatca ttctgtttcc ggttccgttc 960
cagggccaca tcaacccgat tctgcaactg gcgaacgtgc tgtacagcaa gggttttagc 1020
atcaccattt ttcacaccaa cttcaacaag ccgaaaacca gcaactatcc gcacttcacc 1080
tttcgtttca tcttggacaa cgatccgcag gacgagcgta ttagcaacct gccgacccat 1140
ggtccgctgg cgggtatgcg tatcccgatc attaacgagc acggcgcgga tgaactgcgt 1200
cgtgagctgg aactgctgat gctggcgagc gaggaagacg aggaagttag ctgcctgatt 1260
accgatgcgc tgtggtactt cgcgcaaagc gtggcggaca gcctgaacct gcgtcgtctg 1320
gttctgatga ccagcagcct gtttaacttc cacgcgcacg tgagcctgcc gcagtttgac 1380
gagcttggct acctggatcc ggacgattaa 1410

<210> 92
<211> 469

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 92
Met Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys
1 5 10 15
Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu
20 25 30
Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile
35 40 45
Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile
50 55 60
Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu
65 70 75 80
Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe Gln
85 90 95
Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe Gly
100 105 110
Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly
115 120 125
Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly Phe
130 135 140
Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu Gly
145 150 155 160
Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu Ala
165 170 175
His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly Thr
180 185 190
Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly
195 200 205
Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val
210 215 220
Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala
225 230 235 240
Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn
245 250 255
Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu Met Lys Gly Gly
260 265 270
Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
275 280 285
Glu His His His His His His Gly Gly Ser Gly Met Glu Asn Lys Thr
290 295 300
Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu Phe Pro Val Pro Phe
305 310 315 320
Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu Tyr Ser
325 330 335
Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys Pro Lys
340 345 350
Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp Asn Asp
355 360 365
Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala
370 375 380

Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg
385 390 395 400
Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val
405 410 415
Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala
420 425 430
Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe
435 440 445
Asn Phe His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr
450 455 460
Leu Asp Pro Asp Asp
465

<210> 93
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 93
atgctggagg aacaagcgag cggtttcccg atgctgaagg ttaaagatat caagagcgcg 60
tatagcaact ggcagatcct gaaagaaatt ctgggcaaga tgatcaagca gacccgtgcg 120
agcagcggtg tgatttggaa cagctttaaa gagctggagg aaagcgagct ggaaaccgtt 180
atccgtgaaa ttccggcgcc gagcttcctg attccgctgc cgaagcacct gaccgcgagc 240
agcagcagcc tgctggacca cgatcgtacc gtgttccagt ggctggacca gcaaccgccg 300
agcagcgtgc tgtacgttag ctttggcagc cagagcgagg tggacgaaaa ggatttcctg 360
gagattgcgc gtggtctggt tgacagcaaa caaagctttc tgtggcgcgt tcgtccgggc 420
ttcgtgaagg gtagcgagtg ggttgagccg ctgccggatg gttttctggg cgaacgtggt 480
cgtatcgtga agtctgttcc gcaacaagaa gtgctggcgc acggcgcgat tggtgcgttc 540
tggacccaca gcggttggaa cggcaccctg gagagcgtgt gcgaaggcgt tccgatgatc 600
tttagcgact tcggtctgga tcagccgctg aacgcgcgtt acatgagcga tgttctgaaa 660
gtgggcgttt atctggagaa cggctgggag cgtggtgaaa tcgcgaacgc gattcgtcgt 720
gtgatggttg acgaggaagg tgagtacatc cgtcagaacg cgcgtgttct gaagcaaaaa 780
gcggatgtta gcctgatgaa gggtggcagc agctacgaga gcctggaaag cctggttagc 840
tatattagca gcctcgagca tcaccatcac catcacggtg gcagcggtat ggagaacaaa 900
accgaaacca ccgtgcgtcg tcgtcgtatc attctgtttc cggttccgtt ccagggccac 960
atcaacccga ttctgcaact ggcgaacgtg ctgtacagca agggttttag catcaccatt 1020
tttcacacca acttcaacaa gccgaaaacc agcaactatc cgcacttcac ctttcgtttc 1080
atcttggaca acgatccgca ggacgagcgt attagcaacc tgccgaccca tggtccgctg 1140
gcgggtatgc gtatcccgat cattaacgag cacggcgcgg atgaactgcg tcgtgagctg 1200
gaactgctga tgctggcgag cgaggaagac gaggaagtta gctgcctgat taccgatgcg 1260
ctgtggtact tcgcgcaaag cgtggcggac agcctgaacc tgcgtcgtct ggttctgatg 1320
accagcagcc tgtttaactt ccacgcgcac gtgagcctgc cgcagtttga cgagcttggc 1380
tacctggatc cggacgataa aacccgttaa 1410

<210> 94
<211> 469
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 94
Met Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp
1 5 10 15
Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly
20 25 30
Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser
35 40 45
Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile
50 55 60
Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser
65 70 75 80
Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp
85 90 95
Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser
100 105 110
Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp
115 120 125
Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly
130 135 140
Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly
145 150 155 160
Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala
165 170 175
Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser
180 185 190
Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln
195 200 205
Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr
210 215 220
Leu Glu Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg
225 230 235 240
Val Met Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val
245 250 255
Leu Lys Gln Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr
260 265 270
Glu Ser Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu Glu His His
275 280 285
His His His His Gly Gly Ser Gly Met Glu Asn Lys Thr Glu Thr Thr
290 295 300
Val Arg Arg Arg Arg Ile Ile Leu Phe Pro Val Pro Phe Gln Gly His
305 310 315 320
Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu Tyr Ser Lys Gly Phe
325 330 335
Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys Pro Lys Thr Ser Asn
340 345 350
Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp Asn Asp Pro Gln Asp
355 360 365
Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg
370 375 380
Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu
385 390 395 400
Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu
405 410 415

Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu
420 425 430
Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe Asn Phe His
435 440 445
Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro
450 455 460
Asp Asp Lys Thr Arg
465

<210> 95
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 95
atgagcaact ggcagatcct gaaagaaatt ctgggcaaga tgatcaagca gacccgtgcg 60
agcagcggtg tgatttggaa cagctttaaa gagctggagg aaagcgagct ggaaaccgtt 120
atccgtgaaa ttccggcgcc gagcttcctg attccgctgc cgaagcacct gaccgcgagc 180
agcagcagcc tgctggacca cgatcgtacc gtgttccagt ggctggacca gcaaccgccg 240
agcagcgtgc tgtacgttag ctttggcagc cagagcgagg tggacgaaaa ggatttcctg 300
gagattgcgc gtggtctggt tgacagcaaa caaagctttc tgtggcgcgt tcgtccgggc 360
ttcgtgaagg gtagcgagtg ggttgagccg ctgccggatg gttttctggg cgaacgtggt 420
cgtatcgtga agtctgttcc gcaacaagaa gtgctggcgc acggcgcgat tggtgcgttc 480
tggacccaca gcggttggaa cggcaccctg gagagcgtgt gcgaaggcgt tccgatgatc 540
tttagcgact tcggtctgga tcagccgctg aacgcgcgtt acatgagcga tgttctgaaa 600
gtgggcgttt atctggagaa cggctgggag cgtggtgaaa tcgcgaacgc gattcgtcgt 660
gtgatggttg acgaggaagg tgagtacatc cgtcagaacg cgcgtgttct gaagcaaaaa 720
gcggatgtta gcctgatgaa gggtggcagc agctacgaga gcctggaaag cctggttagc 780
tatattagca gcctcgagca tcaccatcac catcacggtg gcagcggtat ggagaacaaa 840
accgaaacca ccgtgcgtcg tcgtcgtatc attctgtttc cggttccgtt ccagggccac 900
atcaacccga ttctgcaact ggcgaacgtg ctgtacagca agggttttag catcaccatt 960
tttcacacca acttcaacaa gccgaaaacc agcaactatc cgcacttcac ctttcgtttc 1020
atcttggaca acgatccgca ggacgagcgt attagcaacc tgccgaccca tggtccgctg 1080
gcgggtatgc gtatcccgat cattaacgag cacggcgcgg atgaactgcg tcgtgagctg 1140
gaactgctga tgctggcgag cgaggaagac gaggaagtta gctgcctgat taccgatgcg 1200
ctgtggtact tcgcgcaaag cgtggcggac agcctgaacc tgcgtcgtct ggttctgatg 1260
accagcagcc tgtttaactt ccacgcgcac gtgagcctgc cgcagtttga cgagcttggc 1320
tacctggatc cggacgataa aacccgtctg gaggaacaag cgagcggttt cccgatgctg 1380
aaggttaaag atatcaagag cgcgtattaa 1410

<210> 96
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 96
Met Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys

1 5 10 15
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
20 25 30
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
35 40 45
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
50 55 60
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
65 70 75 80
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
85 90 95
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
100 105 110
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
115 120 125
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
130 135 140
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
145 150 155 160
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
165 170 175
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
180 185 190
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
195 200 205
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
210 215 220
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
225 230 235 240
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
245 250 255
Ser Leu Val Ser Tyr Ile Ser Ser Leu Glu His His His His His His
260 265 270
Gly Gly Ser Gly Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg
275 280 285
Arg Ile Ile Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile
290 295 300
Leu Gln Leu Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile
305 310 315 320
Phe His Thr Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe
325 330 335
Thr Phe Arg Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser
340 345 350
Asn Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile
355 360 365
Asn Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met
370 375 380
Leu Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala
385 390 395 400
Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg
405 410 415
Leu Val Leu Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser
420 425 430
Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr
435 440 445

Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp
450 455 460
Ile Lys Ser Ala Tyr
465

<210> 97
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 97
atgatcctga aagaaattct gggcaagatg atcaagcaga cccgtgcgag cagcggtgtg 60
atttggaaca gctttaaaga gctggaggaa agcgagctgg aaaccgttat ccgtgaaatt 120
ccggcgccga gcttcctgat tccgctgccg aagcacctga ccgcgagcag cagcagcctg 180
ctggaccacg atcgtaccgt gttccagtgg ctggaccagc aaccgccgag cagcgtgctg 240
tacgttagct ttggcagcca gagcgaggtg gacgaaaagg atttcctgga gattgcgcgt 300
ggtctggttg acagcaaaca aagctttctg tggcgcgttc gtccgggctt cgtgaagggt 360
agcgagtggg ttgagccgct gccggatggt tttctgggcg aacgtggtcg tatcgtgaag 420
tctgttccgc aacaagaagt gctggcgcac ggcgcgattg gtgcgttctg gacccacagc 480
ggttggaacg gcaccctgga gagcgtgtgc gaaggcgttc cgatgatctt tagcgacttc 540
ggtctggatc agccgctgaa cgcgcgttac atgagcgatg ttctgaaagt gggcgtttat 600
ctggagaacg gctgggagcg tggtgaaatc gcgaacgcga ttcgtcgtgt gatggttgac 660
gaggaaggtg agtacatccg tcagaacgcg cgtgttctga agcaaaaagc ggatgttagc 720
ctgatgaagg gtggcagcag ctacgagagc ctggaaagcc tggttagcta tattagcagc 780
ctcgagcatc accatcacca tcacggtggc agcggtatgg agaacaaaac cgaaaccacc 840
gtgcgtcgtc gtcgtatcat tctgtttccg gttccgttcc agggccacat caacccgatt 900
ctgcaactgg cgaacgtgct gtacagcaag ggttttagca tcaccatttt tcacaccaac 960
ttcaacaagc cgaaaaccag caactatccg cacttcacct ttcgtttcat cttggacaac 1020
gatccgcagg acgagcgtat tagcaacctg ccgacccatg gtccgctggc gggtatgcgt 1080
atcccgatca ttaacgagca cggcgcggat gaactgcgtc gtgagctgga actgctgatg 1140
ctggcgagcg aggaagacga ggaagttagc tgcctgatta ccgatgcgct gtggtacttc 1200
gcgcaaagcg tggcggacag cctgaacctg cgtcgtctgg ttctgatgac cagcagcctg 1260
tttaacttcc acgcgcacgt gagcctgccg cagtttgacg agcttggcta cctggatccg 1320
gacgataaaa cccgtctgga ggaacaagcg agcggtttcc cgatgctgaa ggttaaagat 1380
atcaagagcg cgtatagcaa ctggcagtaa 1410

<210> 98
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 98
Met Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Arg Ala
1 5 10 15
Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu
20 25 30
Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro

35 40 45
Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp
50 55 60
Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu
65 70 75 80
Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu Lys Asp Phe Leu
85 90 95
Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Arg
100 105 110
Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val Glu Pro Leu Pro
115 120 125
Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys Ser Val Pro Gln
130 135 140
Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser
145 150 155 160
Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile
165 170 175
Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser
180 185 190
Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly
195 200 205
Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu
210 215 220
Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser
225 230 235 240
Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser
245 250 255
Tyr Ile Ser Ser Leu Glu His His His His His His Gly Gly Ser Gly
260 265 270
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
275 280 285
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
290 295 300
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
305 310 315 320
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
325 330 335
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
340 345 350
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
355 360 365
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
370 375 380
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
385 390 395 400
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
405 410 415
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
420 425 430
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
435 440 445
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
450 455 460
Tyr Ser Asn Trp Gln
465

<210> 99
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 99
atgcacgatc gtaccgtgtt ccagtggctg gaccagcaac cgccgagcag cgtgctgtac 60
gttagctttg gcagccagag cgaggtggac gaaaaggatt tcctggagat tgcgcgtggt 120
ctggttgaca gcaaacaaag ctttctgtgg cgcgttcgtc cgggcttcgt gaagggtagc 180
gagtgggttg agccgctgcc ggatggtttt ctgggcgaac gtggtcgtat cgtgaagtct 240
gttccgcaac aagaagtgct ggcgcacggc gcgattggtg cgttctggac ccacagcggt 300
tggaacggca ccctggagag cgtgtgcgaa ggcgttccga tgatctttag cgacttcggt 360
ctggatcagc cgctgaacgc gcgttacatg agcgatgttc tgaaagtggg cgtttatctg 420
gagaacggct gggagcgtgg tgaaatcgcg aacgcgattc gtcgtgtgat ggttgacgag 480
gaaggtgagt acatccgtca gaacgcgcgt gttctgaagc aaaaagcgga tgttagcctg 540
atgaagggtg gcagcagcta cgagagcctg gaaagcctgg ttagctatat tagcagcctc 600
gagcatcacc atcaccatca cggtggcagc ggtatggaga acaaaaccga aaccaccgtg 660
cgtcgtcgtc gtatcattct gtttccggtt ccgttccagg gccacatcaa cccgattctg 720
caactggcga acgtgctgta cagcaagggt tttagcatca ccatttttca caccaacttc 780
aacaagccga aaaccagcaa ctatccgcac ttcacctttc gtttcatctt ggacaacgat 840
ccgcaggacg agcgtattag caacctgccg acccatggtc cgctggcggg tatgcgtatc 900
ccgatcatta acgagcacgg cgcggatgaa ctgcgtcgtg agctggaact gctgatgctg 960
gcgagcgagg aagacgagga agttagctgc ctgattaccg atgcgctgtg gtacttcgcg 1020
caaagcgtgg cggacagcct gaacctgcgt cgtctggttc tgatgaccag cagcctgttt 1080
aacttccacg cgcacgtgag cctgccgcag tttgacgagc ttggctacct ggatccggac 1140
gataaaaccc gtctggagga acaagcgagc ggtttcccga tgctgaaggt taaagatatc 1200
aagagcgcgt atagcaactg gcagatcctg aaagaaattc tgggcaagat gatcaagcag 1260
acccgtgcga gcagcggtgt gatttggaac agctttaaag agctggagga aagcgagctg 1320
gaaaccgtta tccgtgaaat tccggcgccg agcttcctga ttccgctgcc gaagcacctg 1380
accgcgagca gcagcagcct gctggactaa 1410

<210> 100
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 100
Met His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser
1 5 10 15
Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu Lys
20 25 30
Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser Phe
35 40 45
Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val Glu
50 55 60
Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys Ser

65 70 75 80
Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe Trp
85 90 95
Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly Val
100 105 110
Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg
115 120 125
Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly Trp
130 135 140
Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu
145 150 155 160
Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala
165 170 175
Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser
180 185 190
Leu Val Ser Tyr Ile Ser Ser Leu Glu His His His His His His Gly
195 200 205
Gly Ser Gly Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg
210 215 220
Ile Ile Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu
225 230 235 240
Gln Leu Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe
245 250 255
His Thr Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr
260 265 270
Phe Arg Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn
275 280 285
Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn
290 295 300
Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu
305 310 315 320
Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu
325 330 335
Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu
340 345 350
Val Leu Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu
355 360 365
Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg
370 375 380
Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile
385 390 395 400
Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys
405 410 415
Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe
420 425 430
Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro
435 440 445
Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser
450 455 460
Ser Ser Leu Leu Asp
465

<210> 101
<211> 1410

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 101
atggatcgta ccgtgttcca gtggctggac cagcaaccgc cgagcagcgt gctgtacgtt 60
agctttggca gccagagcga ggtggacgaa aaggatttcc tggagattgc gcgtggtctg 120
gttgacagca aacaaagctt tctgtggcgc gttcgtccgg gcttcgtgaa gggtagcgag 180
tgggttgagc cgctgccgga tggttttctg ggcgaacgtg gtcgtatcgt gaagtctgtt 240
ccgcaacaag aagtgctggc gcacggcgcg attggtgcgt tctggaccca cagcggttgg 300
aacggcaccc tggagagcgt gtgcgaaggc gttccgatga tctttagcga cttcggtctg 360
gatcagccgc tgaacgcgcg ttacatgagc gatgttctga aagtgggcgt ttatctggag 420
aacggctggg agcgtggtga aatcgcgaac gcgattcgtc gtgtgatggt tgacgaggaa 480
ggtgagtaca tccgtcagaa cgcgcgtgtt ctgaagcaaa aagcggatgt tagcctgatg 540
aagggtggca gcagctacga gagcctggaa agcctggtta gctatattag cagcctcgag 600
catcaccatc accatcacgg tggcagcggt atggagaaca aaaccgaaac caccgtgcgt 660
cgtcgtcgta tcattctgtt tccggttccg ttccagggcc acatcaaccc gattctgcaa 720
ctggcgaacg tgctgtacag caagggtttt agcatcacca tttttcacac caacttcaac 780
aagccgaaaa ccagcaacta tccgcacttc acctttcgtt tcatcttgga caacgatccg 840
caggacgagc gtattagcaa cctgccgacc catggtccgc tggcgggtat gcgtatcccg 900
atcattaacg agcacggcgc ggatgaactg cgtcgtgagc tggaactgct gatgctggcg 960
agcgaggaag acgaggaagt tagctgcctg attaccgatg cgctgtggta cttcgcgcaa 1020
agcgtggcgg acagcctgaa cctgcgtcgt ctggttctga tgaccagcag cctgtttaac 1080
ttccacgcgc acgtgagcct gccgcagttt gacgagcttg gctacctgga tccggacgat 1140
aaaacccgtc tggaggaaca agcgagcggt ttcccgatgc tgaaggttaa agatatcaag 1200
agcgcgtata gcaactggca gatcctgaaa gaaattctgg gcaagatgat caagcagacc 1260
cgtgcgagca gcggtgtgat ttggaacagc tttaaagagc tggaggaaag cgagctggaa 1320
accgttatcc gtgaaattcc ggcgccgagc ttcctgattc cgctgccgaa gcacctgacc 1380
gcgagcagca gcagcctgct ggaccactaa 1410

<210> 102
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 102
Met Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser
1 5 10 15
Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu Lys Asp
20 25 30
Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu
35 40 45
Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val Glu Pro
50 55 60
Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys Ser Val
65 70 75 80
Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr
85 90 95
His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly Val Pro

100 105 110
Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr
115 120 125
Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu
130 135 140
Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu
145 150 155 160
Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp
165 170 175
Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu
180 185 190
Val Ser Tyr Ile Ser Ser Leu Glu His His His His His His Gly Gly
195 200 205
Ser Gly Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile
210 215 220
Ile Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln
225 230 235 240
Leu Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His
245 250 255
Thr Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe
260 265 270
Arg Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu
275 280 285
Pro Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu
290 295 300
His Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala
305 310 315 320
Ser Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp
325 330 335
Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val
340 345 350
Leu Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro
355 360 365
Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu
370 375 380
Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys
385 390 395 400
Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met
405 410 415
Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys
420 425 430
Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala
435 440 445
Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser
450 455 460
Ser Leu Leu Asp His
465

<210> 103
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 103
atgccgatga tctttagcga cttcggtctg gatcagccgc tgaacgcgcg ttacatgagc 60
gatgttctga aagtgggcgt ttatctggag aacggctggg agcgtggtga aatcgcgaac 120
gcgattcgtc gtgtgatggt tgacgaggaa ggtgagtaca tccgtcagaa cgcgcgtgtt 180
ctgaagcaaa aagcggatgt tagcctgatg aagggtggca gcagctacga gagcctggaa 240
agcctggtta gctatattag cagcctcgag catcaccatc accatcacgg tggcagcggt 300
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 360
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 420
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 480
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 540
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 600
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 660
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 720
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 780
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 840
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 900
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 960
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 1020
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 1080
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 1140
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 1200
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 1260
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1320
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1380
accctggaga gcgtgtgcga aggcgtttaa 1410

<210> 104
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 104
Met Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
1 5 10 15
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
20 25 30
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
35 40 45
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
50 55 60
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
65 70 75 80
Ser Leu Val Ser Tyr Ile Ser Ser Leu Glu His His His His His His
85 90 95
Gly Gly Ser Gly Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg
100 105 110
Arg Ile Ile Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile
115 120 125
Leu Gln Leu Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile

130 135 140
Phe His Thr Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe
145 150 155 160
Thr Phe Arg Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser
165 170 175
Asn Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile
180 185 190
Asn Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met
195 200 205
Leu Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala
210 215 220
Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg
225 230 235 240
Leu Val Leu Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser
245 250 255
Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr
260 265 270
Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp
275 280 285
Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly
290 295 300
Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser
305 310 315 320
Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile
325 330 335
Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser
340 345 350
Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp
355 360 365
Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser
370 375 380
Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp
385 390 395 400
Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly
405 410 415
Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly
420 425 430
Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala
435 440 445
Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser
450 455 460
Val Cys Glu Gly Val
465

<210> 105
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 105
atgtgggagc gtggtgaaat cgcgaacgcg attcgtcgtg tgatggttga cgaggaaggt 60

gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 120
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctcgagcat 180
caccatcacc atcacggtgg cagcggtatg gagaacaaaa ccgaaaccac cgtgcgtcgt 240
cgtcgtatca ttctgtttcc ggttccgttc cagggccaca tcaacccgat tctgcaactg 300
gcgaacgtgc tgtacagcaa gggttttagc atcaccattt ttcacaccaa cttcaacaag 360
ccgaaaacca gcaactatcc gcacttcacc tttcgtttca tcttggacaa cgatccgcag 420
gacgagcgta ttagcaacct gccgacccat ggtccgctgg cgggtatgcg tatcccgatc 480
attaacgagc acggcgcgga tgaactgcgt cgtgagctgg aactgctgat gctggcgagc 540
gaggaagacg aggaagttag ctgcctgatt accgatgcgc tgtggtactt cgcgcaaagc 600
gtggcggaca gcctgaacct gcgtcgtctg gttctgatga ccagcagcct gtttaacttc 660
cacgcgcacg tgagcctgcc gcagtttgac gagcttggct acctggatcc ggacgataaa 720
acccgtctgg aggaacaagc gagcggtttc ccgatgctga aggttaaaga tatcaagagc 780
gcgtatagca actggcagat cctgaaagaa attctgggca agatgatcaa gcagacccgt 840
gcgagcagcg gtgtgatttg gaacagcttt aaagagctgg aggaaagcga gctggaaacc 900
gttatccgtg aaattccggc gccgagcttc ctgattccgc tgccgaagca cctgaccgcg 960
agcagcagca gcctgctgga ccacgatcgt accgtgttcc agtggctgga ccagcaaccg 1020
ccgagcagcg tgctgtacgt tagctttggc agccagagcg aggtggacga aaaggatttc 1080
ctggagattg cgcgtggtct ggttgacagc aaacaaagct ttctgtggcg cgttcgtccg 1140
ggcttcgtga agggtagcga gtgggttgag ccgctgccgg atggttttct gggcgaacgt 1200
ggtcgtatcg tgaagtctgt tccgcaacaa gaagtgctgg cgcacggcgc gattggtgcg 1260
ttctggaccc acagcggttg gaacggcacc ctggagagcg tgtgcgaagg cgttccgatg 1320
atctttagcg acttcggtct ggatcagccg ctgaacgcgc gttacatgag cgatgttctg 1380
aaagtgggcg tttatctgga gaacggctaa 1410

<210> 106
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 106
Met Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
1 5 10 15
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
20 25 30
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
35 40 45
Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu Glu His His His His His
50 55 60
His Gly Gly Ser Gly Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg
65 70 75 80
Arg Arg Ile Ile Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro
85 90 95
Ile Leu Gln Leu Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr
100 105 110
Ile Phe His Thr Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His
115 120 125
Phe Thr Phe Arg Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile
130 135 140
Ser Asn Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile
145 150 155 160
Ile Asn Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu

165 170 175
Met Leu Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp
180 185 190
Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg
195 200 205
Arg Leu Val Leu Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val
210 215 220
Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys
225 230 235 240
Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys
245 250 255
Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu
260 265 270
Gly Lys Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn
275 280 285
Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu
290 295 300
Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala
305 310 315 320
Ser Ser Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu
325 330 335
Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln
340 345 350
Ser Glu Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val
355 360 365
Asp Ser Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys
370 375 380
Gly Ser Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg
385 390 395 400
Gly Arg Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu Ala His Gly
405 410 415
Ala Ile Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu
420 425 430
Ser Val Cys Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp
435 440 445
Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val
450 455 460
Tyr Leu Glu Asn Gly
465

<210> 107
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 107
atgcgtggtg aaatcgcgaa cgcgattcgt cgtgtgatgg ttgacgagga aggtgagtac 60
atccgtcaga acgcgcgtgt tctgaagcaa aaagcggatg ttagcctgat gaagggtggc 120
agcagctacg agagcctgga aagcctggtt agctatatta gcagcctcga gcatcaccat 180
caccatcacg gtggcagcgg tatggagaac aaaaccgaaa ccaccgtgcg tcgtcgtcgt 240
atcattctgt ttccggttcc gttccagggc cacatcaacc cgattctgca actggcgaac 300

gtgctgtaca gcaagggttt tagcatcacc atttttcaca ccaacttcaa caagccgaaa 360
accagcaact atccgcactt cacctttcgt ttcatcttgg acaacgatcc gcaggacgag 420
cgtattagca acctgccgac ccatggtccg ctggcgggta tgcgtatccc gatcattaac 480
gagcacggcg cggatgaact gcgtcgtgag ctggaactgc tgatgctggc gagcgaggaa 540
gacgaggaag ttagctgcct gattaccgat gcgctgtggt acttcgcgca aagcgtggcg 600
gacagcctga acctgcgtcg tctggttctg atgaccagca gcctgtttaa cttccacgcg 660
cacgtgagcc tgccgcagtt tgacgagctt ggctacctgg atccggacga taaaacccgt 720
ctggaggaac aagcgagcgg tttcccgatg ctgaaggtta aagatatcaa gagcgcgtat 780
agcaactggc agatcctgaa agaaattctg ggcaagatga tcaagcagac ccgtgcgagc 840
agcggtgtga tttggaacag ctttaaagag ctggaggaaa gcgagctgga aaccgttatc 900
cgtgaaattc cggcgccgag cttcctgatt ccgctgccga agcacctgac cgcgagcagc 960
agcagcctgc tggaccacga tcgtaccgtg ttccagtggc tggaccagca accgccgagc 1020
agcgtgctgt acgttagctt tggcagccag agcgaggtgg acgaaaagga tttcctggag 1080
attgcgcgtg gtctggttga cagcaaacaa agctttctgt ggcgcgttcg tccgggcttc 1140
gtgaagggta gcgagtgggt tgagccgctg ccggatggtt ttctgggcga acgtggtcgt 1200
atcgtgaagt ctgttccgca acaagaagtg ctggcgcacg gcgcgattgg tgcgttctgg 1260
acccacagcg gttggaacgg caccctggag agcgtgtgcg aaggcgttcc gatgatcttt 1320
agcgacttcg gtctggatca gccgctgaac gcgcgttaca tgagcgatgt tctgaaagtg 1380
ggcgtttatc tggagaacgg ctgggagtaa 1410

<210> 108
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Circular Permuted Variant of SEQ ID NO: 32

<400> 108
Met Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu
1 5 10 15
Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala
20 25 30
Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser
35 40 45
Leu Val Ser Tyr Ile Ser Ser Leu Glu His His His His His His Gly
50 55 60
Gly Ser Gly Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg
65 70 75 80
Ile Ile Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu
85 90 95
Gln Leu Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe
100 105 110
His Thr Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr
115 120 125
Phe Arg Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn
130 135 140
Leu Pro Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn
145 150 155 160
Glu His Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu
165 170 175
Ala Ser Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu
180 185 190
Trp Tyr Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu

195 200 205
Val Leu Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu
210 215 220
Pro Gln Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg
225 230 235 240
Leu Glu Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile
245 250 255
Lys Ser Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys
260 265 270
Met Ile Lys Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe
275 280 285
Lys Glu Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro
290 295 300
Ala Pro Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser
305 310 315 320
Ser Ser Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln
325 330 335
Gln Pro Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu
340 345 350
Val Asp Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser
355 360 365
Lys Gln Ser Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser
370 375 380
Glu Trp Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg
385 390 395 400
Ile Val Lys Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile
405 410 415
Gly Ala Phe Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val
420 425 430
Cys Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro
435 440 445
Leu Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu
450 455 460
Glu Asn Gly Trp Glu
465

<210> 109
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 109
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg cggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540

ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 110
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 110
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Ala Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 111
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 111
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgggaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 112
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 112
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Gly Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 113
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 113
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 114
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 114
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 115
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 115
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtgc gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 116
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 116
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Ala Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 117
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 117
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatccagaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaaggggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 118
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 118
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Gln Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 119
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 119
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgataaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 120
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 120
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80

His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Asp Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 121
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 121
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgct gaagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 122
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 122
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 123
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 123
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180

acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 124
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 124
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 125
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 125
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agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatgctgaaa 600

gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 126
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 126
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
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Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Met Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 127
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 127
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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatctcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 128
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 128
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 129
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc aggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
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tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 130
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 130
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Gln Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 131
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

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agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agggcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
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ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
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<210> 132
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 132
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Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 133
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

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acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
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ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gtctctgaaa 600
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cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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<210> 134
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 134
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 135
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 135
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcaagaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 136
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 136
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 137
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 137
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgt tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 138
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 138
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 139
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 139
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240

catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 140
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 140
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 141
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 141
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg ttgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 142
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 142
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 143
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 143
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca ggttctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 144
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 144
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Val Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 145
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 145
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg cggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 146
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 146
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Ala Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 147
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 147
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ttcgctggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 148
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 148
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Ala Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys

420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 149
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 149
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccttggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 150
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 150
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Leu Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 151
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 151
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 152
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 152
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 153
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 153
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggtgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 154
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 154
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe

145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 155
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 155
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ttccatggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300

cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 156
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 156
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe His Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 157
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 157
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720

ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 158
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 158
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 159
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 159
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtggggtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 160
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 160
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Gly Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 161
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 161
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccgacggat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 162

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 162
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Thr Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 163
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 163
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 164
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 164
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430

Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 165
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 165
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtgggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 166
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 166
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 167

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 167
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgatgttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 168
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 168
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu

100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Met Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 169
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 169
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 170
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 170
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160

Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 171
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 171
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360

attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttaggct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 172
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 172
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 173
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 173
atggagaaca aaacccctac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780

cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggggaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 174
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 174
Met Glu Asn Lys Thr Pro Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 175
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 175
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcctcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 176
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 176
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 177
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 177
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 178
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 178
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 179
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 179
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
tggaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 180
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 180

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Trp Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 181
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 181
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaatctct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 182
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 182
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 183
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 183
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctggg gctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 184
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 184
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110

Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Gly Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 185
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 185

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggctc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 186
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 186
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ser Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 187
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 187
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 188
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 188
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 189
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 189
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agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctgtcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 190
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 190
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ser Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 191
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 191
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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cctaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260

tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 192
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 192
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 193
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 193
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgaggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 194
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 194
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 195
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 195
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcgggtggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
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tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
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<210> 196
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 196
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Gly Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 197
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 197
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agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 198
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 198
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 199
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 199
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaactct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 200
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 200
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 201
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 201
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60

ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcggc ggttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 202
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 202
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 203
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 203
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc cgatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480

gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 204
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 204
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 205
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 205
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccaggat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 206
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 206
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gln Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 207
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 207
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cataccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 208
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 208
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp His Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 209
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 209
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccc tgaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 210
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 210
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 211
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 211
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 212
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 212
Met Glu Asn Pro Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 213
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 213
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atcagagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 214
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 214
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr

65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Gln Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 215
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 215
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaggtct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 216
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 216
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Gly Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 217
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 217
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaagatct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 218
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 218
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Asp Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 219
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 219
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540

ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
gcgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 220
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 220
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Ala Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 221
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 221
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 222
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 222
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 223
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 223
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 224
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 224
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 225
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 225
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atcggagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 226
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 226
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Arg Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 227
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 227
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaaggggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 228
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 228
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Ala
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 229
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 229
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 230
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 230
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 231
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 231
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 232
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 232
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 233
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 233
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180

acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 234
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 234
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190

Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 235
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 235
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg tcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600

gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 236
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 236
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Val Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 237
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 237
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 238
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 238
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 239
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 239
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 240
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 240
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 241
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 241
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 242
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 242
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 243
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 243
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 244
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 244
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 245
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 245
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 246
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 246
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 247
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 247
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 248
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 248
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 249
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 249
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240

catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 250
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 250
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 251
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 251
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcaaaaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
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accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
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<210> 252
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 252
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 253
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 253
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 254
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 254
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 255
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 255
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 256
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 256
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 257
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 257
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 258
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 258
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys

420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 259
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 259
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 260
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 260
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 261
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 261
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 262
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 262
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 263
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 263
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 264
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 264
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 265
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 265
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300

cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 266
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 266
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 267
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 267
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720

ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 268
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 268
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 269
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 269
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 270
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 270
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 271
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 271
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccaggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 272

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 272
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 273
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 273
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 274
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase variant of SEQ ID NO: 32

<400> 274
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430

Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 275
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 275
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 276
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 276
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 277

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 277
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcagcaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 278
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 278
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu

100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 279
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 279
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 280
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 280
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160

Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 281
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 281
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360

attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 282
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 282
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 283
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 283
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780

cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 284
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 284
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 285
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 285
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 286
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 286
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 287
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 287
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 288
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 288
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 289
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 289
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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 290
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 290

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 291
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 291
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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgaac gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 292
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 292
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 293
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 293
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
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ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 294
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 294
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110

Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 295
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 295

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
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tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 296
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 296
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 297
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 297
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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 298
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 298
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 299
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 299
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcaaaaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 300
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 300
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 301
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 301
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260

tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 302
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 302
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 303
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 303
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 304
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 304
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 305
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 305
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 306
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 306
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 307
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 307
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 308
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 308
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 309
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 309
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagtcgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 310
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 310
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 311
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 311
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 312
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 312
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 313
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 313
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480

gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcaaaaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 314
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 314
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 315
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 315
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 316
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 316
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 317
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 317
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 318
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 318
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 319
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 319
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 320
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 320
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 321
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 321
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 322
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 322
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 323
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 323
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 324
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 324
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr

65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 325
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 325
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 326
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 326
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 327
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 327
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ttccagggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 328
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 328
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala

180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 329
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 329
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540

ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcagcaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 330
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 330
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ser Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 331
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 331
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 332
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 332
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 333
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 333
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgtgcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 334
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 334
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Cys Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 335
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 335
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 336
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 336
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 337
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 337
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 338
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 338
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 339
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 339
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtca tcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcgcgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttgtgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 340
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 340
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80

His Gly Pro Leu Ala Gly His Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Val Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 341
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 341
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgct taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 342
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 342
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Leu Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 343
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 343
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180

acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 344
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 344
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 345
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 345
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgg tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gagcaaaaaa 600

gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacagcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 346
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 346
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Val Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Lys Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Ser Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 347
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 347
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 348
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 348
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 349
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 349
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 350
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 350
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 351
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 351
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 352
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 352
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 353
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 353
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 354
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 354
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 355
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 355
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 356
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 356
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 357
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 357
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 358
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 358
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 359
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 359
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240

catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
tatatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
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<210> 360
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 360
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 361
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 361
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 362
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 362
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 363
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 363
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gtaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 364
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 364
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 365
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 365
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 366
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 366
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 367
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 367
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 368
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 368
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 369
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 369
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 370
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 370
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 371
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 371
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 372
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 372
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 373
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 373
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 374
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 374
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe

145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 375
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 375
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300

cgtcgtgagc tggaaaccct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gtaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 376
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 376
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 377
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 377
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720

ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggc gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaatgcacg tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 378
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 378
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 379
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 379
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 380
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 380
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 381
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 381
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa tcggtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 382

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 382
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 383
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 383
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 384
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 384
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 385
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 385
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 386
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 386
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 387

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 387
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gtaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcact tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 388
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 388
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu

100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 389
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 389
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 390
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 390
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160

Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 391
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 391
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360

attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 392
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 392
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 393
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 393
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780

cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 394
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 394
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 395
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 395
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 396
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 396
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 397
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 397
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
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accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 398
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 398
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 399
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 399
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
tatatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 400
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 400

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 401
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 401
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 402
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 402
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 403
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 403
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 404
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 404
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 405
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 405

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 406
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 406
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 407
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 407
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggc gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 408
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 408
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 409
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 409
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 410
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 410
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 411
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 411
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260

gtgatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 412
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 412
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 413
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 413
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 414
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 414
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 415
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 415
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgct tgttctgaag gacaaagcgg atgttagcct gatgcctggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 416
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 416
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 417
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 417
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa tcggtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 418
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 418
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 419
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 419
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 420
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 420
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 421
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 421
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga agaaggtgag 1260
gtgatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 422
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 422
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 423
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 423
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480

gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 424
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 424
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 425
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 425
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 426
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 426
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 427
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 427
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 428
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 428
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 429
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 429
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gtaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcacg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 430
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 430
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 431
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 431
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cggaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 432
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 432
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 433
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 433
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 434
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 434
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 435
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 435
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 436
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 436
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 437
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 437
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 438
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 438
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 439
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 439
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540

ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 440
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 440
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 441
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 441
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgcctggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 442
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 442
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 443
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 443
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 444
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 444
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 445
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 445
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 446
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 446
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 447
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 447
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cggaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 448
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 448
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 449
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 449
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 450
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 450
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 451
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 451
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cggaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 452
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 452
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 453
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 453
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 454
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 454
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 455
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 455
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa tcggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600

gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 456
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 456
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 457
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 457
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 458
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 458
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 459
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 459
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 460
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 460
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 461
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 461
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 462
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 462
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 463
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 463
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tatatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 464
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 464
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 465
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 465
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gtaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgcctggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 466
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 466
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 467
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 467
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cggaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 468
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 468
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 469
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 469
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240

catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 470
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 470
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 471
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 471
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 472
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 472
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 473
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 473
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcggc tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 474
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 474
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 475
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 475
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gtaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 476
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 476
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 477
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 477
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa tcggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 478
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 478
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 479
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 479
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cggaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 480
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 480
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 481
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 481
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cggaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 482
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 482
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 483
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 483
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgcctggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 484
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 484
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe

145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 485
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 485
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300

cgtcgtgagc tggaaagcct gatgcgggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcggttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgtccggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctagaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 486
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 486
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 487
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 487
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcggcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720

ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcggc tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 488
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 488
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 489
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 489
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 490
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 490
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 491
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 491
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacag agaaggtgag 1260
tatatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 492

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 492
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Tyr Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 493
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 493
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtc ctatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacgc agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag gacaaagcgg atgttagcct gatgcctggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 494
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 494
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Pro
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Ala Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Met Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 495
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 495
atggagaaca aaaccgaaac taccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agccctgaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgct tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 496
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 496
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Leu Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 497

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 497
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaaccct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgttaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttagac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttacct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga agaaggtgag 1260
gtgatccgtc agaacgcgct tgttctgaag gacaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 498
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 232

<400> 498
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Thr Leu Met Leu Ala Ser Glu

100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Leu Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 499
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 499
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 500
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 500
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 501
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 501
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 502
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 502
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 503
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 503
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780

ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 504
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 504
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 505
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 505
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 506
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 506
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 507
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 507
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agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 508
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 508
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 509
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 509
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 510
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 510

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 511
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 511
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtagagagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg gctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atcgtagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 512
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 512
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Arg Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 513
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 513
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgattcgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 514
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 514
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110

Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 515
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 515

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtaaagagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg gctgcctcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggacagtgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaatctgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgaatgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtagaa tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 516
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 516
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Lys Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 517
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 517
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtatag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattt 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420

ctggttctga tgaccagcag cttgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagctag gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggtggac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 518
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 518
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 519
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 519
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agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt ttcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 520
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 520
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 521
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 521
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ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
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ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260

gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 522
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 522
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 523
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 523
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
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ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatgcgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 524
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 524
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Met Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 525
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 525
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agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gcctgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
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agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
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ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 526
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 526
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 527
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 527
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaac cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaatta 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cttgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagctag gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttca gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ttgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtctga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 528
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 528
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Pro Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 529
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 529
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtaaagagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctggcc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgaatgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgaaagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 530
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 530
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Lys Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Ala Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Glu Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 531
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 531
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggtgccg 60

ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgcctaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt ttcagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgattcgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 532
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 532
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 533
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 533
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgcctaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt ttcagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaat cgtttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
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accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccattcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatgcgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 534
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 534
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Met Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 535
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 535
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg gctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccgggcgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 536
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 536
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 537
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 537
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt ttcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatgcgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 538
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 538
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Gly Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Met Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 539
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 539
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggacgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggatgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc aaaacgcgcg tgttctgaag caaaaagcgg atcaaagcct ggccaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct t 1371

<210> 540
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 540
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400

Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 541
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 541
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggacgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgatgttt 480
gacgagcttg gctacctgga tccgtcggat aaaaccggtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcag 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtg aaaacgcgcg tgttctgaag caaaaagcgg atgtcagcct ggccaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct t 1371

<210> 542
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 542
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Gly Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Glu Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 543
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 543
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcgggcg agcgaggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccattcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatgcgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
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<210> 544
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 544
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Met Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 545
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 545
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaattact gatgcggggc agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg gcaagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccctgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtg 960
gagcctctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgttcgact ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
gtgatccgtc agaacgcgcg tgttctgaag caaaaagcgg atggtagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 546
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 348

<400> 546
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Arg Gly Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Pro Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Arg Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Val Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Gly Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 547
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase SEQ ID NO: 500 without histidine tag

<400> 547
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ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
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<210> 548
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase SEQ ID NO: 500 without histidine tag

<400> 548
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 549
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 549
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 550
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 550
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 551
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 551
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggtagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
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<210> 552
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 552
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 553
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 553
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agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgtgagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 554
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 554
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 555
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 555
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaatta 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgaca gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcaaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 556
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 556
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 557
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 557
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattt 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 558
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 558
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 559
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 559
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 560
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 560
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 561
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 561
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 562
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 562
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 563
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 563
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc gccggaattt 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt ttcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 564
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 564
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 565
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 565
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccgagtgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600

gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 566
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 566
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 567
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 567
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgattcgtc aaaacgcggc ggttctgaag gataaagcgg atcaaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 568
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 568
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 569
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 569
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattt 300
cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctggca gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcaaagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 570
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 570
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Ala Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 571
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 571
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caaaggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtattccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgagtgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 572
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 572
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 573
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 573
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gcgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggactccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcgaagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 574
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 574
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 575
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 575
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaac cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 576
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 576
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Pro Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 577
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 577
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggactccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcaaagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 578
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 578
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 579
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 579
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240

catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaatta 300
cgtagagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 580
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 580
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 581
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 581
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caaaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc gccggaattt 300
cgtagagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 582
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 582
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Arg Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 583
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 583
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaattt 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 584
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 584
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Glu Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 585
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 585
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caaaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgaca gcgagcagca gcagcctgct ggactccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 586
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 586
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 587
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 587
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattt 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 588
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 588
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 589
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 589
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caaaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaatta 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtg aaaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 590
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 590
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Glu Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 591
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 591
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 592
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 592
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 593
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 593
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaaccggtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctggca gcgagcagca gcagcctgct ggactccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 594
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 594
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Gly Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Ala Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 595
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 595
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300

cgtcgtgagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgattcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 596
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 596
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 597
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 597
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaac cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaatta 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720

ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 598
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 598
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Pro Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 599
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 599
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaatta 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctggca gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 600
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 600
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Leu Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Ala Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 601
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 601
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaatta 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 602

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 602
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Pro Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 603
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 603
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccaatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgaca gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 604
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 604
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 605
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 605
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 606
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 606
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Glu Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 607

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 607
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc gccggaattt 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt ttcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtg aaaacgcggc ggttctgaag gataaagcgg atcgaagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 608
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 608
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Pro Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Glu Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 609
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 609
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 610
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 610
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 611
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 611
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaaccggtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgattcgtg aaaacgcggc ggttctgaag gataaagcgg atgagagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 612
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 612
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Gly Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Glu Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Glu Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 613
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 613
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaattt 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780

ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 614
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 614
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Glu Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 615
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 615
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 616
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 616
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Glu Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 617
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 617
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt ttcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgagagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcaaagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 618
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 618
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 619
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 619
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccgggtgat aaaaccggtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctggca gcgagcagca gcagcctgct ggaccccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 620
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 620

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Gly Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Ala Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Pro Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 621
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 621
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggactccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 622
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 622
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 623
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 623
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caaaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgaca gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 624
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 624
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 625
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 625

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 626
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 626
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gly Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 627
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 627
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgattcgtc aaaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 628
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 628
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 629
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 629
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgattcgtc aaaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 630
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 630
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 631
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 631
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260

gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcaaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 632
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 632
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 633
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 633
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaattc 300
cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgaa ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 634
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 634
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Glu Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 635
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 635
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgatgttt 480
ttagagcttg gctacctgga tccgagtgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 636
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 636
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 637
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 637
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattt 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaaccggtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgc gaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 638
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 638
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Gly Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 639
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 639
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaattc 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt ttcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgatgttt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggactccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgaa ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 640
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 640
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 641
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 641
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaaccggtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 642
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 642
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Gly Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 643
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 643
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaattt 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480

ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 644
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 644
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 645
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 645
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caaaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattt 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtg aaaacgcggc ggttctgaag gataaagcgg atcaaagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 646
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 646
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Glu Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 647
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 647
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcaaagcct gatgaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 648
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 648
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 649
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 649
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaatta 300
cgtagagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 650
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 650
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Pro Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 651
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 651
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggactccgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 652
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 652
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 653
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 653
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 654
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 654
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 655
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 655
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaac cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 656
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 656
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Pro Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 657
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 657
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgaca gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgaa ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 658
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 658
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 659
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 659
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgaca gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 660
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 660
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 661
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 661
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 662
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 662
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 663
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 663
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 664
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 664
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 665
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 665
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatac gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgaca gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgattcgtc aaaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 666
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 666
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 667
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 667
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc gccggaattt 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaagttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 668
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 668
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Pro Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 669
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 669
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 670
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 670
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 671
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 671
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaac cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 672
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 672
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Pro Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 673
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 673
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa cgagcaacta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaatta 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtggcgct gccgatgttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctggca gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaagcgat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtg aaaacgcggc ggttctgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 674
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 674
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ala Leu Pro Met Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Ala Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Glu Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 675
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 675
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600

gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgggagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 676
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 676
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gly Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 677
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 677
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 678
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 678
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 679
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 679
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaac cgagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatccgtc agaacgcggc ggttctgaag gataaagcgg atgttagcct gatgaatggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 680
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 548

<400> 680
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Pro Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Ile Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Met Asn Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 681
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 681
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat tgccggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaatcagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 682
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 682

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 683
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 683
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgct taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 684
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 684
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Leu Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 685
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 685
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat tgaccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 686
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 686
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Asp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 687
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 687
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat tgcccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 688
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 688
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 689
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 689
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240

catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat tgccggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaatcagaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 690
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 690
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Ala

195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 691
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 691
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatgaaaaaa 600
gaaattctgg ataagatgct tgaccagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgtggc ggttctgaag gataaagcgg atcggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 692
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 692
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Met Lys Lys Glu Ile Leu Asp Lys Met Leu Asp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Val Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 693
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 693
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggcg gattaaaaaa 600
gaaattctgg ataagatgat taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 694
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 694
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 695
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 695
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 696
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 696
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 697
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 697
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccgctgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgct tgcccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 698
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 698
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Leu Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Leu Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 699
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 699
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat tgccggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 700
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 700
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 701
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 701
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggcg gattaaaaaa 600
gaaattctgg ataagatgct taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 702
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 702
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Lys Lys Glu Ile Leu Asp Lys Met Leu Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 703
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 703
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggcg gattaaaaaa 600
gaaattctgg ataagatgct tgaccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 704
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 704
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Lys Lys Glu Ile Leu Asp Lys Met Leu Asp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 705
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 705
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggcg gattaaaaaa 600
gaaattctgg ataagatgat tgcccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagaa ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 706
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 706
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 707
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 707
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 708
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 708
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 709
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 709
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgct taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 710
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 710
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Leu Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 711
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 711
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 712

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 712
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 713
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 713
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 714
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 714
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 715
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 715
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcaccg ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggcg gattaaaaaa 600
gaaattctgg ataagatgat tgaccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt ggcttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 716
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 716
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Asp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Gly Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 717

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 717
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 718
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 718
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 719
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 719
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccgctgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatgaaaaaa 600
gaaattctgg ataagatgat tgcccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gccttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 720
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 720
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Leu Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Met Lys Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 721
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 721
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccgggcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 722
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 722
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 723
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 723
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780

ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagaa ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 724
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 724
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 725
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 725
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatgaaaaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc tgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaatcagat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 726
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 726
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Met Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Leu Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 727
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 727
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat tgcccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 728
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 728
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 729
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 729
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggcg gatgaaaaaa 600
gaaattctgg ataagatgat tgacggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 730
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 730

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Arg Met Lys Lys Glu Ile Leu Asp Lys Met Ile Asp
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 731
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 731
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatggcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaatg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 732
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 732
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Met Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 733
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 733
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgct tgcccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaatcagaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 734
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 734
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Leu Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 735
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 735

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 736
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 736
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 737
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 737
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccgctgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattaaaaaa 600
gaaattctgg ataagatgat taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 738
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 738
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Leu Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 739
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 739
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 740
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 740
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 741
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 741
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgagcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgct tgcccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 742
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 742
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Ser Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Leu Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 743
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 743
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcaccg tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctggg actgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggcg gattgcgaaa 600
gaaattctgg ataagatgat taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaatcagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 744
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 744
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Gly Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 745
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 745
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggcgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggcg gattaaaaaa 600
gaaattctgg ataagatgct tgaccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 746
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 746
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Lys Lys Glu Ile Leu Asp Lys Met Leu Asp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 747
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 747
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggtgccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcggggc agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggcg gatggcgaaa 600
gaaattctgg ataagatgct tgaccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaatcagaa ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 748
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 748
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Gly Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Arg Met Ala Lys Glu Ile Leu Asp Lys Met Leu Asp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Ser Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 749
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 749
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgatgttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggcg gattaaaaaa 600
gaaattctgg ataagatgct taaaggaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 750
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 750
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Met Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Arg Ile Lys Lys Glu Ile Leu Asp Lys Met Leu Lys
195 200 205
Gly Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 751
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 751
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggtct gcgtatcccg atccttaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggcg gatgaaaaaa 600
gaaattctgg ataagatgat tgaccagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttcaa 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 752
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 752
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Leu Arg Ile Pro Ile Leu Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Arg Met Lys Lys Glu Ile Leu Asp Lys Met Ile Asp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gln Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 753
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 753
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggattagcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaattggca gatcgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 754
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 562

<400> 754
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 755
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> codon-optimized Oryza Sativa Japonica glycosyltransferase

<400> 755
atgcaccatc atcatcatca tggcggtagc ggcatggata gcggctatag cagctcctac 60
gccgcagcag caggtatgca cgtcgtcatt tgcccgtggc ttgcgtttgg ccatttactt 120
ccgtgcctgg acctcgctca gcgtttagca agccgtggtc atcgcgtgag ctttgtgagc 180
actccacgca atattagccg tttaccacca gttcgtccag cacttgcacc actggttgca 240
ttcgttgcac tgccactgcc acgtgttgaa ggtctgccag atggtgcaga aagcaccaac 300
gatgtgccac atgatcgtcc agacatggtt gaattacatc gtcgcgcctt tgatggtctg 360
gccgcaccat tcagtgagtt cctgggtact gcatgtgcag attgggttat cgttgacgtg 420
tttcatcatt gggcagcagc agcagcgctc gaacacaagg tgccatgcgc gatgatgctg 480
ctgggcagcg cgcacatgat cgcgtcaatc gcagatcgtc gtctggaacg tgcggaaact 540
gaaagtccag cagcagcagg tcaaggtcgt ccagcagcag caccaacttt tgaagtcgcg 600
cgcatgaaac tgatccgcac taaaggtagt agtggcatgt ctttagcgga acgttttagc 660
ctgaccctga gccgtagcag tttagtggtt ggtcgtagtt gcgtcgagtt cgaaccagaa 720
acggttccgc tgttatcaac tctgcgcggt aaacctatta cctttcttgg cttaatgccg 780
cccttacatg aaggtcgtcg tgaagatggt gaagacgcaa ctgttcgttg gcttgacgca 840
cagccagcaa aaagcgttgt ctatgtcgca ctgggtagtg aagtgccgtt aggtgtggaa 900

aaagtccatg aactggctct gggcctggag ttagctggga ctcgtttcct gtgggcactg 960
cgcaaaccaa ctggtgttag cgatgcagat ctgctgccag cgggttttga agaacgcacc 1020
cgtggtcgtg gtgttgtcgc aactcgttgg gtgccgcaga tgtcgattct tgcacatgca 1080
gcagttggtg cgttcctgac ccattgcggt tggaacagca ccattgaagg cctgatgttc 1140
ggtcatccac tgatcatgct gccgatcttc ggtgatcaag gcccgaatgc gcgtctgatc 1200
gaggcgaaaa acgcgggttt acaggttgcg cgcaatgatg gtgatggcag tttcgatcgc 1260
gaaggtgttg cggcggctat ccgcgcggtt gcagtggaag aagaaagcag caaggtgttt 1320
caggcaaagg cgaaaaagct gcaagagatc gttgcggata tggcatgtca cgaacgctac 1380
attgatggtt tcatccagca gctgcgtagt tacaaagact aa 1422

<210> 756
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> codon-optimized Oryza Sativa Japonica glycosyltransferase

<400> 756
Met His His His His His His Gly Gly Ser Gly Met Asp Ser Gly Tyr
1 5 10 15
Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His Val Val Ile Cys Pro
20 25 30
Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu Asp Leu Ala Gln Arg
35 40 45
Leu Ala Ser Arg Gly His Arg Val Ser Phe Val Ser Thr Pro Arg Asn
50 55 60
Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu Ala Pro Leu Val Ala
65 70 75 80
Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly Leu Pro Asp Gly Ala
85 90 95
Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro Asp Met Val Glu Leu
100 105 110
His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro Phe Ser Glu Phe Leu
115 120 125
Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp Val Phe His His Trp
130 135 140
Ala Ala Ala Ala Ala Leu Glu His Lys Val Pro Cys Ala Met Met Leu
145 150 155 160
Leu Gly Ser Ala His Met Ile Ala Ser Ile Ala Asp Arg Arg Leu Glu
165 170 175
Arg Ala Glu Thr Glu Ser Pro Ala Ala Ala Gly Gln Gly Arg Pro Ala
180 185 190
Ala Ala Pro Thr Phe Glu Val Ala Arg Met Lys Leu Ile Arg Thr Lys
195 200 205
Gly Ser Ser Gly Met Ser Leu Ala Glu Arg Phe Ser Leu Thr Leu Ser
210 215 220
Arg Ser Ser Leu Val Val Gly Arg Ser Cys Val Glu Phe Glu Pro Glu
225 230 235 240
Thr Val Pro Leu Leu Ser Thr Leu Arg Gly Lys Pro Ile Thr Phe Leu
245 250 255
Gly Leu Met Pro Pro Leu His Glu Gly Arg Arg Glu Asp Gly Glu Asp
260 265 270
Ala Thr Val Arg Trp Leu Asp Ala Gln Pro Ala Lys Ser Val Val Tyr

275 280 285
Val Ala Leu Gly Ser Glu Val Pro Leu Gly Val Glu Lys Val His Glu
290 295 300
Leu Ala Leu Gly Leu Glu Leu Ala Gly Thr Arg Phe Leu Trp Ala Leu
305 310 315 320
Arg Lys Pro Thr Gly Val Ser Asp Ala Asp Leu Leu Pro Ala Gly Phe
325 330 335
Glu Glu Arg Thr Arg Gly Arg Gly Val Val Ala Thr Arg Trp Val Pro
340 345 350
Gln Met Ser Ile Leu Ala His Ala Ala Val Gly Ala Phe Leu Thr His
355 360 365
Cys Gly Trp Asn Ser Thr Ile Glu Gly Leu Met Phe Gly His Pro Leu
370 375 380
Ile Met Leu Pro Ile Phe Gly Asp Gln Gly Pro Asn Ala Arg Leu Ile
385 390 395 400
Glu Ala Lys Asn Ala Gly Leu Gln Val Ala Arg Asn Asp Gly Asp Gly
405 410 415
Ser Phe Asp Arg Glu Gly Val Ala Ala Ala Ile Arg Ala Val Ala Val
420 425 430
Glu Glu Glu Ser Ser Lys Val Phe Gln Ala Lys Ala Lys Lys Leu Gln
435 440 445
Glu Ile Val Ala Asp Met Ala Cys His Glu Arg Tyr Ile Asp Gly Phe
450 455 460
Ile Gln Gln Leu Arg Ser Tyr Lys Asp
465 470

<210> 757
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum tuberosum glycosyltransferase

<400> 757
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccgtttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgcctaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgttg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc tggattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140

gttgcaatgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattacggaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 758
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum tuberosum glycosyltransferase

<400> 758
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320

Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Met Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Thr Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 759
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum tuberosum glycosyltransferase

<400> 759
atgcaccatc atcatcatca tggcggtagc ggcatggcaa ccttgcgcgt tctgatgttt 60
ccgtggctcg cgtatggaca tatctctcct ttcctgaatg tagcaaaaaa actggccgac 120
cgtgggttcc tgatttattt gtgtagtact ccgattaatt tgaagagcac catcaagaag 180
atcccggaga aatatgcaga tagcatccag ctgatcgagt tacacctgcc agaactgccg 240
gaattaccac cacattatca taccaccaac ggttttccgc cacatctgaa caacaccctg 300
cataaagccc tggagatgag caagccgaac tttagcaaga tcctgcaaaa cctgaagccg 360
gacctggtta tttacgatat gctgcaacag tgggcagaac atgtcgcgaa tgaacagaac 420
atcccagcgg tgaaactgat taccttcggt gcagcagtct ttagctacct gttctacctg 480
gttaagaagc cggaagcagt gtttccgttt cccgcgatta acctgtcgaa gatcgaacag 540
gaaaagatgt acgcgaaaga cttcgaagac cgcttggttg acggcaacat ccagatcatg 600
ctcattagca ccagtcgtac cattgaagcg aagtacattg atcactgtac cgagctgatt 660
aattggaagg tggtgccggt tggtccgcca gtgcaggacc caatcacgaa caacgcggat 720
gataaggagc tgatggattg gcttggtact aaagacgaga acagcaccgt gtttgtgagc 780
tttggcagcg aatatttcct gagcaaggaa gatatggaag aagttgcatt tggcctggaa 840
ctcagtaatg tgaacttcat ctgggtggca cgctttccga aaggcgaaga tcaaaatctg 900
gaagatgcgt taccgaaagg cttcctggaa cgtattggtg aacgtggtcg cgtactggat 960
aagtttgcgc cgcagccacg cattctgaac catccgagca ccggcggttt catctcgcat 1020
tgcggttgga acagcgtaat ggagagcgtg gatttcggtg ttccgatcat cgcaatgccg 1080
atccagtacg atcagccgtc aaatgcacgt ctgatcgtgg agctgggtgt tgcggttgag 1140
attgttcgcg acgatgatgg caagattcac cgtggtgaaa tcgcggaaac cctgaaggat 1200
gtgattaccg gcaaaaccgg cgaaaatctg cgcggtaaag tacgcgacat tagcaagaac 1260
ctgaagtcaa tccgcggtga ggagatggac accgcggcgg aagtgcttat ccagctgtgt 1320
aagaacagca acgagtgtaa gtaa 1344

<210> 760

<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum tuberosum glycosyltransferase

<400> 760
Met His His His His His His Gly Gly Ser Gly Met Ala Thr Leu Arg
1 5 10 15
Val Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu
20 25 30
Asn Val Ala Lys Lys Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys
35 40 45
Ser Thr Pro Ile Asn Leu Lys Ser Thr Ile Lys Lys Ile Pro Glu Lys
50 55 60
Tyr Ala Asp Ser Ile Gln Leu Ile Glu Leu His Leu Pro Glu Leu Pro
65 70 75 80
Glu Leu Pro Pro His Tyr His Thr Thr Asn Gly Phe Pro Pro His Leu
85 90 95
Asn Asn Thr Leu His Lys Ala Leu Glu Met Ser Lys Pro Asn Phe Ser
100 105 110
Lys Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Met Leu
115 120 125
Gln Gln Trp Ala Glu His Val Ala Asn Glu Gln Asn Ile Pro Ala Val
130 135 140
Lys Leu Ile Thr Phe Gly Ala Ala Val Phe Ser Tyr Leu Phe Tyr Leu
145 150 155 160
Val Lys Lys Pro Glu Ala Val Phe Pro Phe Pro Ala Ile Asn Leu Ser
165 170 175
Lys Ile Glu Gln Glu Lys Met Tyr Ala Lys Asp Phe Glu Asp Arg Leu
180 185 190
Val Asp Gly Asn Ile Gln Ile Met Leu Ile Ser Thr Ser Arg Thr Ile
195 200 205
Glu Ala Lys Tyr Ile Asp His Cys Thr Glu Leu Ile Asn Trp Lys Val
210 215 220
Val Pro Val Gly Pro Pro Val Gln Asp Pro Ile Thr Asn Asn Ala Asp
225 230 235 240
Asp Lys Glu Leu Met Asp Trp Leu Gly Thr Lys Asp Glu Asn Ser Thr
245 250 255
Val Phe Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Lys Glu Asp Met
260 265 270
Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe Ile Trp
275 280 285
Val Ala Arg Phe Pro Lys Gly Glu Asp Gln Asn Leu Glu Asp Ala Leu
290 295 300
Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly Arg Val Leu Asp
305 310 315 320
Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser Thr Gly Gly
325 330 335
Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Val Asp Phe
340 345 350
Gly Val Pro Ile Ile Ala Met Pro Ile Gln Tyr Asp Gln Pro Ser Asn
355 360 365
Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val Arg Asp

370 375 380
Asp Asp Gly Lys Ile His Arg Gly Glu Ile Ala Glu Thr Leu Lys Asp
385 390 395 400
Val Ile Thr Gly Lys Thr Gly Glu Asn Leu Arg Gly Lys Val Arg Asp
405 410 415
Ile Ser Lys Asn Leu Lys Ser Ile Arg Gly Glu Glu Met Asp Thr Ala
420 425 430
Ala Glu Val Leu Ile Gln Leu Cys Lys Asn Ser Asn Glu Cys Lys
435 440 445

<210> 761
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<223> codon-optimized Lycium barbarum glycosyltransferase

<400> 761
atgcaccatc atcatcatca tggcggtagc ggcatgggca ccgaagtcac ggttcataaa 60
aacaccctgc gcgttctgat gtttccgtgg ttagcctatg gtcatattag cccgttcctg 120
aatgtcgcga aaaagctggt tgatcgtggc ttcctgatct acctgtgcag cacggcgatt 180
aacctgaaga gcaccatcaa gaagatcccg gagaaatata gcgatagcat tcagctgatc 240
gagttacacc tgccagaatt accggaactg ccaccacatt atcatactac caacggttta 300
ccaccgcatc tgaaccatac cctgcaaaaa gccctgaaga tgagcaagcc gaactttagc 360
aagatcctgc aaaacctgaa gccggacctg gttatttacg atctgctcca gcagtgggcg 420
gaaggtgtgg ctaacgaaca gaacatcccg gctgtgaagt tgttaacaag tggtgcagcg 480
gttctgagct actttttcaa cctggttaaa aaaccgggtg tcgaatttcc gtttccggct 540
atctacctgc gcaaaaacga gctggaaaag atgagcgaac tgctcgcaca aagcgcaaaa 600
gacaaagaac cagacggtgt tgatccattc gctgatggca acatgcaggt catgctgatg 660
agcacttcgc gcattattga ggcgaagtac attgactact ttagcggcct gtcaaattgg 720
aaagtggttc cagttggtcc gccggtgcaa gatccaattg cggatgatgc agacgagatg 780
gaactgattg attggcttgg taaaaaggat gagaatagca ccgtttttgt gagcttcggt 840
agtgagtact tcctgagcaa ggaagaccgc gaagaaattg cattcggtct ggaacttagc 900
aacgttaact tcatctgggt tgcacgtttt ccgaaaggtg aagaacaaaa tctggaagac 960
gctctgccaa aaggtttcct ggaacgtatc ggtgatcgtg gtcgtgttct ggacaagttc 1020
gctccgcagc cgcgcattct gaaccatccg agcaccggtg gttttattag ccattgtggt 1080
tggaatagcg tcatggaaag cgtggatttc ggcgttccaa tcattgcgat gccgattcat 1140
ctggatcagc cgatgaatgc gcgcctgatc gttgaactgg gtgtcgcagt ggagattgtg 1200
cgcgacgact atggcaagat ccatcgcgaa gaaattgcgg agatcctgaa agatgtgatc 1260
gcaggtaaga gcggtgagaa cctgaaggcg aaaatgcgcg acattagcaa gaacctgaag 1320
agcatccgcg acgaagaaat ggacaccgcg gcggaagaac tgatccagct gtgtaagaac 1380
agcccgaagc tgaaataa 1398

<210> 762
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> codon-optimized Lycium barbarum glycosyltransferase

<400> 762

Met His His His His His His Gly Gly Ser Gly Met Gly Thr Glu Val
1 5 10 15
Thr Val His Lys Asn Thr Leu Arg Val Leu Met Phe Pro Trp Leu Ala
20 25 30
Tyr Gly His Ile Ser Pro Phe Leu Asn Val Ala Lys Lys Leu Val Asp
35 40 45
Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Ala Ile Asn Leu Lys Ser
50 55 60
Thr Ile Lys Lys Ile Pro Glu Lys Tyr Ser Asp Ser Ile Gln Leu Ile
65 70 75 80
Glu Leu His Leu Pro Glu Leu Pro Glu Leu Pro Pro His Tyr His Thr
85 90 95
Thr Asn Gly Leu Pro Pro His Leu Asn His Thr Leu Gln Lys Ala Leu
100 105 110
Lys Met Ser Lys Pro Asn Phe Ser Lys Ile Leu Gln Asn Leu Lys Pro
115 120 125
Asp Leu Val Ile Tyr Asp Leu Leu Gln Gln Trp Ala Glu Gly Val Ala
130 135 140
Asn Glu Gln Asn Ile Pro Ala Val Lys Leu Leu Thr Ser Gly Ala Ala
145 150 155 160
Val Leu Ser Tyr Phe Phe Asn Leu Val Lys Lys Pro Gly Val Glu Phe
165 170 175
Pro Phe Pro Ala Ile Tyr Leu Arg Lys Asn Glu Leu Glu Lys Met Ser
180 185 190
Glu Leu Leu Ala Gln Ser Ala Lys Asp Lys Glu Pro Asp Gly Val Asp
195 200 205
Pro Phe Ala Asp Gly Asn Met Gln Val Met Leu Met Ser Thr Ser Arg
210 215 220
Ile Ile Glu Ala Lys Tyr Ile Asp Tyr Phe Ser Gly Leu Ser Asn Trp
225 230 235 240
Lys Val Val Pro Val Gly Pro Pro Val Gln Asp Pro Ile Ala Asp Asp
245 250 255
Ala Asp Glu Met Glu Leu Ile Asp Trp Leu Gly Lys Lys Asp Glu Asn
260 265 270
Ser Thr Val Phe Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Lys Glu
275 280 285
Asp Arg Glu Glu Ile Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
290 295 300
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
305 310 315 320
Ala Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg Val
325 330 335
Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser Thr
340 345 350
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Val
355 360 365
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Leu Asp Gln Pro
370 375 380
Met Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
385 390 395 400
Arg Asp Asp Tyr Gly Lys Ile His Arg Glu Glu Ile Ala Glu Ile Leu
405 410 415
Lys Asp Val Ile Ala Gly Lys Ser Gly Glu Asn Leu Lys Ala Lys Met
420 425 430
Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Asp Glu Glu Met Asp

435 440 445
Thr Ala Ala Glu Glu Leu Ile Gln Leu Cys Lys Asn Ser Pro Lys Leu
450 455 460
Lys
465

<210> 763
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum lycopersicum glycosyltransferase

<400> 763
atgcaccatc atcatcatca tggcggtagc ggcatgagca ccaccctgaa agtactgatg 60
tttccgtttc ttgcgtatgg tcacatttct ccatacctga atgtcgctaa aaaacttgca 120
gaccgtggct ttctcatcta cctgtgcagc accccaatta acctgaaaag caccattaac 180
aagatcccgg agaaatacgc agactctatt cagctgatcg aactgcacct gccagaatta 240
ccggaactgc caccacatta ccacaccact aatggtctgc caccaaatct gaaccatatt 300
ctgcgtcgtg cgttgaagat gagcaaaccg aactttagca agatcatgca gaatctgaaa 360
ccggatctgc tgatctacga tattctccag cagtgggcag aagatgtcgc aactgagctg 420
aacattccgg cggttaaact gttgaccagt ggtgtcgcag tgtttagcta ctttttcaac 480
ctgaccaaaa agcccgaagt ggagttccca tacccggcga tctatctgcg caagatcgaa 540
ctggtacgtt ggtgtgaaac cctgagcaag cacaacaaag aaggcgaaga acatgacgat 600
ggtctggcct atggcaacat gcagatcatg ctgatgagca cgagcaagat cctggaggcg 660
aaatacattg actattgtat cgagctgacc aattggaaag tcgttccggt tggtagttta 720
gtgcaggatt cgattaccaa cgatgcagca gatgacgata tggagttaat tgattggctt 780
ggtactaaag acgagaatag caccgtgttt gtgagctttg gcagcgagta tttcctgagc 840
aaagaagatg ttgaagaagt ggcgttcggt ctggagctga gcaacgtgaa ctttatctgg 900
gttgttcgct ttccgaaagg cgaagaaaaa aatctggaag atgttctgcc aaaaggcttc 960
tttgaacgta ttggcgaacg tggtcgtgtt ctggataagt ttgcgccgca gccacgcatt 1020
ctgaaccatc cgagcacggg tggcttcatt agccattgcg gttggaacag cgcgatggag 1080
agcattgatt ttggcgtccc tatcgtggca atgccgatgc agctggacca gccaatgaat 1140
gcgcgcctga ttgtggagct gggtgttgcg gtggagattg tccgtgacga tgatggcaag 1200
atttaccgcg gagaaattgc ggagaccctg aaaggtgtga tcacgggaga gattggtgag 1260
atcctgcgtg caaaggtgcg tgacattagc aagaacctga aggctatcaa agacgaggag 1320
atggatgtgg cggcgcagga gctgatccag ctgtgtcgca acagcaacaa gtaa 1374

<210> 764
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum lycopersicum glycosyltransferase

<400> 764
Met His His His His His His Gly Gly Ser Gly Met Ser Thr Thr Leu
1 5 10 15
Lys Val Leu Met Phe Pro Phe Leu Ala Tyr Gly His Ile Ser Pro Tyr
20 25 30
Leu Asn Val Ala Lys Lys Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu

35 40 45
Cys Ser Thr Pro Ile Asn Leu Lys Ser Thr Ile Asn Lys Ile Pro Glu
50 55 60
Lys Tyr Ala Asp Ser Ile Gln Leu Ile Glu Leu His Leu Pro Glu Leu
65 70 75 80
Pro Glu Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro Asn
85 90 95
Leu Asn His Ile Leu Arg Arg Ala Leu Lys Met Ser Lys Pro Asn Phe
100 105 110
Ser Lys Ile Met Gln Asn Leu Lys Pro Asp Leu Leu Ile Tyr Asp Ile
115 120 125
Leu Gln Gln Trp Ala Glu Asp Val Ala Thr Glu Leu Asn Ile Pro Ala
130 135 140
Val Lys Leu Leu Thr Ser Gly Val Ala Val Phe Ser Tyr Phe Phe Asn
145 150 155 160
Leu Thr Lys Lys Pro Glu Val Glu Phe Pro Tyr Pro Ala Ile Tyr Leu
165 170 175
Arg Lys Ile Glu Leu Val Arg Trp Cys Glu Thr Leu Ser Lys His Asn
180 185 190
Lys Glu Gly Glu Glu His Asp Asp Gly Leu Ala Tyr Gly Asn Met Gln
195 200 205
Ile Met Leu Met Ser Thr Ser Lys Ile Leu Glu Ala Lys Tyr Ile Asp
210 215 220
Tyr Cys Ile Glu Leu Thr Asn Trp Lys Val Val Pro Val Gly Ser Leu
225 230 235 240
Val Gln Asp Ser Ile Thr Asn Asp Ala Ala Asp Asp Asp Met Glu Leu
245 250 255
Ile Asp Trp Leu Gly Thr Lys Asp Glu Asn Ser Thr Val Phe Val Ser
260 265 270
Phe Gly Ser Glu Tyr Phe Leu Ser Lys Glu Asp Val Glu Glu Val Ala
275 280 285
Phe Gly Leu Glu Leu Ser Asn Val Asn Phe Ile Trp Val Val Arg Phe
290 295 300
Pro Lys Gly Glu Glu Lys Asn Leu Glu Asp Val Leu Pro Lys Gly Phe
305 310 315 320
Phe Glu Arg Ile Gly Glu Arg Gly Arg Val Leu Asp Lys Phe Ala Pro
325 330 335
Gln Pro Arg Ile Leu Asn His Pro Ser Thr Gly Gly Phe Ile Ser His
340 345 350
Cys Gly Trp Asn Ser Ala Met Glu Ser Ile Asp Phe Gly Val Pro Ile
355 360 365
Val Ala Met Pro Met Gln Leu Asp Gln Pro Met Asn Ala Arg Leu Ile
370 375 380
Val Glu Leu Gly Val Ala Val Glu Ile Val Arg Asp Asp Asp Gly Lys
385 390 395 400
Ile Tyr Arg Gly Glu Ile Ala Glu Thr Leu Lys Gly Val Ile Thr Gly
405 410 415
Glu Ile Gly Glu Ile Leu Arg Ala Lys Val Arg Asp Ile Ser Lys Asn
420 425 430
Leu Lys Ala Ile Lys Asp Glu Glu Met Asp Val Ala Ala Gln Glu Leu
435 440 445
Ile Gln Leu Cys Arg Asn Ser Asn Lys
450 455

<210> 765
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum lycopersicum glycosyltransferase

<400> 765
atgcaccatc atcatcatca tggcggtagc ggcatgggga ctcaggtgac ggaacatggt 60
acttctaatc ttcgcgttgt aatgtttccg tggttagcct atggtcatat ttccccattc 120
ctgtacgtcg cgaaaaaact ggctgatcgt ggtttcctga tttacctgtg cagcaccccg 180
attaacctga agagcaccat cgaaaagatt ccggagaaat atgcagactc tatccacctg 240
atcgagctgc atctgccaga actgccggaa ttaccaccgc attaccatac taccaacggt 300
ttaccacccc atctgaacca taccctgcaa aaggcactga agatgagcaa gccgaacctg 360
agcaagatcc tgaagaacct gaagccggat ctgatgatct acgatgtgct gcaacagtgg 420
gcagaacgtg ttgcaaatga acagagcatc ccggcggttc gtctgctgac cttcggtgca 480
gccgtattta gctacttttg taacctggtt aaaaaaccgg gtgtcgaatt tccgtttccc 540
gacatctacc tgcgcaagat cgaacaggtt aaactgggcg agatgctgga aaagagcgcg 600
aaagaccaag acccagacga tgaagaacgt ctggtggatg aatacaagca gattgcactg 660
atctgtacga gccgtaccat tgaggcgaag tacattgatt tcctgcttga attgagcaac 720
ctgaaagtgg ttccagttgg tagtccagtg caggatctga ttaccaatga cgcggatgat 780
atggagctga ttgattggct tggctcaaaa gacgaaaaca gcaccgtttt cgttagcttc 840
ggtagcgagt acttcctgag caaagaagat atggaagaag tggctttagg ccttgaactg 900
agcaatgtga actttgtgtg ggtcgcacgt tttccgaaag gcgaagaaca gaatctggaa 960
gatgcactgc cgaaaggttt cctggaacgc attggtgaac gtggtcgtgt tctggacaag 1020
tttgcgccgc agctgcgtat tctgaaccac acgagcaccg gcggttttat tagccactgt 1080
ggttggaata gcgtcatgga gagcattcac ttcggtgtgc cgattgtggc gatgccgatg 1140
cacctggatc agccgatgaa tgcacgcttg atcgtggagc ttggtgttgc ggtggagatc 1200
gtgcgcgacg acgatggcaa gatttaccgc gaggagatcg cgaaaaccct gaaagatgtg 1260
attaccgagc gcatcggcga aaacctgcgt gctaagatgc gcgagattag caagaacctg 1320
aacagcatta gcggtgaaga aatggacgcg gcggcgcatg aactgatcca gttttgtaag 1380
attagcacca actaa 1395

<210> 766
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum lycopersicum glycosyltransferase

<400> 766
Met His His His His His His Gly Gly Ser Gly Met Gly Thr Gln Val
1 5 10 15
Thr Glu His Gly Thr Ser Asn Leu Arg Val Val Met Phe Pro Trp Leu
20 25 30
Ala Tyr Gly His Ile Ser Pro Phe Leu Tyr Val Ala Lys Lys Leu Ala
35 40 45
Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Pro Ile Asn Leu Lys
50 55 60
Ser Thr Ile Glu Lys Ile Pro Glu Lys Tyr Ala Asp Ser Ile His Leu
65 70 75 80
Ile Glu Leu His Leu Pro Glu Leu Pro Glu Leu Pro Pro His Tyr His

85 90 95
Thr Thr Asn Gly Leu Pro Pro His Leu Asn His Thr Leu Gln Lys Ala
100 105 110
Leu Lys Met Ser Lys Pro Asn Leu Ser Lys Ile Leu Lys Asn Leu Lys
115 120 125
Pro Asp Leu Met Ile Tyr Asp Val Leu Gln Gln Trp Ala Glu Arg Val
130 135 140
Ala Asn Glu Gln Ser Ile Pro Ala Val Arg Leu Leu Thr Phe Gly Ala
145 150 155 160
Ala Val Phe Ser Tyr Phe Cys Asn Leu Val Lys Lys Pro Gly Val Glu
165 170 175
Phe Pro Phe Pro Asp Ile Tyr Leu Arg Lys Ile Glu Gln Val Lys Leu
180 185 190
Gly Glu Met Leu Glu Lys Ser Ala Lys Asp Gln Asp Pro Asp Asp Glu
195 200 205
Glu Arg Leu Val Asp Glu Tyr Lys Gln Ile Ala Leu Ile Cys Thr Ser
210 215 220
Arg Thr Ile Glu Ala Lys Tyr Ile Asp Phe Leu Leu Glu Leu Ser Asn
225 230 235 240
Leu Lys Val Val Pro Val Gly Ser Pro Val Gln Asp Leu Ile Thr Asn
245 250 255
Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Ser Lys Asp Glu
260 265 270
Asn Ser Thr Val Phe Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Lys
275 280 285
Glu Asp Met Glu Glu Val Ala Leu Gly Leu Glu Leu Ser Asn Val Asn
290 295 300
Phe Val Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
305 310 315 320
Asp Ala Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly Arg
325 330 335
Val Leu Asp Lys Phe Ala Pro Gln Leu Arg Ile Leu Asn His Thr Ser
340 345 350
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
355 360 365
Ile His Phe Gly Val Pro Ile Val Ala Met Pro Met His Leu Asp Gln
370 375 380
Pro Met Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
385 390 395 400
Val Arg Asp Asp Asp Gly Lys Ile Tyr Arg Glu Glu Ile Ala Lys Thr
405 410 415
Leu Lys Asp Val Ile Thr Glu Arg Ile Gly Glu Asn Leu Arg Ala Lys
420 425 430
Met Arg Glu Ile Ser Lys Asn Leu Asn Ser Ile Ser Gly Glu Glu Met
435 440 445
Asp Ala Ala Ala His Glu Leu Ile Gln Phe Cys Lys Ile Ser Thr Asn
450 455 460

<210> 767
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>

<223> codon-optimized Solanum lycopersicum glycosyltransferase

<400> 767
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgtgca gcggcgctgc gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaaa cgcagtatga acgttttccg 240
ggctatcatg cggttaaagg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccattg gaacgcgtat catggcgcga ccgcggtgag cgcgagcatg 480
accggctttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccatg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcaaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggcttcggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagcg cgaaaagcct aaccgcgggt ttttttgcgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcgc gtgaatggtt tccgcatggt 960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagtca ggaaagataa agcgagcaaa gccccgtttg gtggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattg tgcgtgcgct gggccagagc 1260
gtggcgctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgttcgcg gaagtggcg 1359

<210> 768
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> codon-optimized Solanum lycopersicum glycosyltransferase

<400> 768
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Cys Ser Gly Ala Ala Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Thr Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Val Lys Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr His Trp Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Phe Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala His Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ala Lys Ser Leu Thr
275 280 285
Ala Gly Phe Phe Ala Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Arg Glu Trp Phe Pro His Gly
305 310 315 320
Phe Thr Thr Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Val Arg
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Gly Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Val Arg Ala
405 410 415
Leu Gly Gln Ser Val Ala Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 769
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 769
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240

ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 770
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 770
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr

195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 771
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 771
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccggttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatccacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660

accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgtgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 772
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 772
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile His Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255

Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 773
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 773
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccggttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgtgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080

attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 774
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 774
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly

305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 775
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 775
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaagga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 776
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 776
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365

Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 777
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 777
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccgttta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcagaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgcctaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcggctggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgttg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc tggattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcaatgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattacggaa 1200
accctgaaag atgtgattac cggcgaaact ggtgaggtcc tgcgcggcaa agtacgagac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 778
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 778
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Gly Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Met Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Thr Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Val Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu

420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 779
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 779
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccgttta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgcctaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcggctggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgttg acgacatggg actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc tggattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcaatgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattacggaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgagac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 780
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 780
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser

35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Gly Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Gly Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Met Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Thr Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 781
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 781
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccgttta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcagaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgcctaaagt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcggctggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgttg acgacccaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatcctag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc tggattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcaatgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattacggaa 1200
accctgaaag atgtgattac cggcaaaact ggtgaggtcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 782
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 782
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95

His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Gly Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Pro Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Met Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Thr Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Lys Thr Gly Glu Val Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 783
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 783
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccgttta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgtccaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgcctaaagt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcggctggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgttg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatcctag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc tggattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcaatgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattacggaa 1200
accctgaaag atgtgattac cggcaaaact ggtgagatcc tgcgcggcaa agtacgagac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 784
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 784
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Ser Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu

145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Gly Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Met Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Thr Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Lys Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 785
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 785
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccgtttt gtggagctga cactgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300

aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgcctaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agtggttccg gttggtccgc catttcagga cccgattact 720
aatgatgttg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccagat ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc tggattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcaatgg agatcgtgcg tgatgacgat ggcaacattc accgcgaaga aattacggaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa gcctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 786
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 786
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Phe Val Glu Leu Thr Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205

Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Asp Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Met Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Glu Glu Ile Thr Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Ser Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 787
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 787
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccgtttt gtggagctga cactgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatctacc tgcctaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agtggttccg gttggtccgc catttcagga cccgattact 720

aatgatgttg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc tggattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcaatgg agatcgtgcg tgatgacgat ggcaacattc accgcgaaga aattacggaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 788
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosyltransferase Variant of SEQ ID NO: 758

<400> 788
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Arg Phe Val Glu Leu Thr Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Tyr Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Val Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser

260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Met Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Glu Glu Ile Thr Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 789
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 789
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140

gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 790
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 790
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320

Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 791
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 791
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 792

<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 792
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu

370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 793
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 793
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 794
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 794
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430

Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 795
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 795
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat tagcccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 796
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 796
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45

Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 797

<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 797
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat tagcccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt gtttgggtgg cgcgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 798
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 798
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys

100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Val Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 799
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 799
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat tagcccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atttgggtgg tgcgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 800
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 800
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160

Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Val Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 801
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 801
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360

ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 802
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 802
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser

210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 803
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 803
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780

gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 804
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 804
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270

Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 805
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 805
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgt gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200

accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 806
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 806
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro

325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 807
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 807
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 808
<211> 451

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 808
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380

Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 809
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 809
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg ttggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 810
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 810

Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Val Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn

435 440 445
Lys Tyr Lys
450

<210> 811
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 811
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgg cgtttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 812
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 812
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr

50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 813
<211> 1356

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 813
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc ttggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 814
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 814
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110

Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 815
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 815

atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat tctgccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 816
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 816
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Leu Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys

165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 817
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 817
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420

ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtctttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 818
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 818
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220

Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 819
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 819
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840

ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 820
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 820
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val

275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 821
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 821
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgacgaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260

attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 822
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 822
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335

Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Thr Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 823
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 823
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat tgggccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 824
<211> 451
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 824
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Gly Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu

385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 825
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 825
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgtgtatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 826
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 826
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val

1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Cys
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445

Lys Tyr Lys
450

<210> 827
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 827
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acggttttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 828
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 828
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60

Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Gly Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 829
<211> 1353
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 829
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtggttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 830
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 830
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln

115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Trp Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 831
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 831
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60

tggcttgcgt atggtcatat ttctccgttt ttgagtatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 832
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 832
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175

Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 833
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 833
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480

aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ttggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 834
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 834
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr

225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 835
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 835
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900

gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgctgaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 836
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 836
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285

Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Leu Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 837
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 837
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgcggatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320

atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 838
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 838
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Arg
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu

340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 839
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 839
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgg gttttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 840
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 840
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Gly Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400

Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 841
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 841
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 842
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 842
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15

Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys

450

<210> 843
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 843
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
gtgatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 844
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 844
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu

65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Val Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 845
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 845
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat taagccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 846
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 846
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Lys Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125

Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 847
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 847
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120

ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 848
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 848
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu

180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 849
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 849
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540

aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 850
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 850
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240

Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 851
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 851
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960

cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 852
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 852
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu

290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 853
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 853
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 854
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 854
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350

Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 855
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 855
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 856
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 856
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly

405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 857
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 857
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 858
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 858
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn

20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 859
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 859
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 860
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 860
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80

Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 861
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 861
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 862
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 862
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys

130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 863
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 863
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180

ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 864
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 864
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190

Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 865
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 865
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600

atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 866
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 866
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp

245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 867
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 867
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020

ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 868
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 868
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300

Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 869
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 869
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 870
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 870
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp

355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 871
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 871
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 872
<211> 451
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 872
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415

Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 873
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 873
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 874
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 874
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30

Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 875
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 875
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaagga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 876
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 876
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn

85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 877
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 877
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 878
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 878
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140

Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 879
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 879
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240

ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 880
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 880
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr

195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 881
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 881
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660

accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaagga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 882
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 882
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255

Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 883
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 883
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080

attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 884
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 884
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly

305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 885
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 885
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 886
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 886
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365

Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 887
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 887
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 888
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 888
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu

420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 889
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 889
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 890
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 890
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser

35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 891
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 891
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 892
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 892
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95

His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 893
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 893
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga gattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 894
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 894
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu

145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 895
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 895
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300

aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 896
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 896
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205

Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 897
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 897
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagttt gtggagctgc atttgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720

aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 898
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 898
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser

260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 899
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 899
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140

gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 900
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 900
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320

Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 901
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 901
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 902

<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 902
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu

370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 903
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 903
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 904
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 904
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430

Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 905
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 905
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 906
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 906
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45

Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 907

<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 907
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaagga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 908
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 908
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys

100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 909
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 909
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 910
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 910
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160

Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 911
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 911
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360

ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 912
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 912
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser

210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 913
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 913
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatctc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780

gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtgcgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 914
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 914
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270

Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 915
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 915
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaagga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200

accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 916
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 916
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro

325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 917
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 917
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatattg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgggttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgccgtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgagag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 918
<211> 451

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 918
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380

Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Arg Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 919
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 919
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccatttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaagga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 920
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 920

Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn

435 440 445
Lys Tyr Lys
450

<210> 921
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 921
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccatttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 922
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 922
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr

50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 923
<211> 1353

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 923
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 924
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 924
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110

Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 925
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 925

atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 926
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 926
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys

165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 927
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 927
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420

ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 928
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 928
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220

Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 929
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 929
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840

ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 930
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 930
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val

275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 931
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 931
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatattg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260

attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 932
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 932
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335

Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 933
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 933
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 934
<211> 451
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 934
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu

385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 935
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 935
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 936
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 936
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val

1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445

Lys Tyr Lys
450

<210> 937
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 937
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttc gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 938
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 938
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60

Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 939
<211> 1353
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 939
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 940
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 940
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln

115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 941
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 941
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60

tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 942
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 942
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175

Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 943
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 943
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480

aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgattcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 944
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 944
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr

225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ile His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 945
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 945
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900

gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 946
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 946
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285

Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 947
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 947
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccagtta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaagga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320

atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 948
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 948
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile Gln Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu

340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 949
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 949
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 950
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 950
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400

Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 951
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 951
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcaccat caagaagatc 180
ccggagaaat acagtgagag catccattta gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 952
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 952
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15

Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Thr Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys

450

<210> 953
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 953
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 954
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 954
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu

65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 955
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 955
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 956
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 956
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125

Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 957
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 957
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120

ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 958
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 958
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu

180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 959
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 959
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540

aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 960
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 960
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240

Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 961
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 961
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960

cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 962
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 962
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu

290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 963
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 963
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 964
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 964
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350

Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 965
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 965
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 966
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 966
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly

405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 967
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 967
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgagcaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 968
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 968
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn

20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 969
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 969
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaaagcttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg aggttgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 970
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 970
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80

Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Val Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 971
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 971
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 972
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 972
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys

130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 973
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 973
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180

ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaaagcttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accgttagag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 974
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 974
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190

Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Val Arg Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 975
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 975
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600

atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 976
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 976
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp

245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 977
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 977
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gagattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020

ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 978
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 978
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300

Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 979
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 979
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatcta 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 980
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 980
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp

355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 981
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 981
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaaagcttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttagag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 982
<211> 451
<212> PRT
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 982
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Arg Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415

Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 983
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 983
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaaagcttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 984
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 984
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30

Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 985
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 985
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc actattgagg ctaagtacct ggactatcta 660
accgaactga gcaattggaa agttgttccg gttggtccgc cgtttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggta ccaaagacga gaacagtacc 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 986
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 986
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn

85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 987
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>

<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 987
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaaagcttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg agattgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
acccttagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 988
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 988
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140

Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 989
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 989
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240

ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc actattgagg ctaagtacct ggactatcta 660
accgaactga gcaattggaa agttgttccg gttggtccgc cgtttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 990
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 990
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr

195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 991
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 991
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gagattgagg ctaagtacct ggactatcta 660

accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttagata ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcctttctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 992
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 992
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255

Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Leu Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 993
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 993
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gagattgagg ctaagtacct ggactatcta 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacc 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aacaaatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080

attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 994
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 994
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Gln Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly

305 310 315 320
Arg Val Val Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 995
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 995
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatcta 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 996
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 996
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365

Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 997
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 997
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc actattgagg ctaagtacct ggactatcta 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 998
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 998
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu

420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 999
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 999
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt taggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaaagcttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agattgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accgttaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcgaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1000
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 792

<400> 1000
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser

35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Val Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Glu Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1001
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1001
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1002
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1002
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95

His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1003
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1003
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgccgtgg aggttgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1004
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1004
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu

145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Val Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1005
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1005
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300

aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1006
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1006
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205

Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1007
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1007
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720

aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgccgtgg aggttgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1008
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1008
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser

260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Val Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1009
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1009
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140

gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1010
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1010
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320

Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1011
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1011
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattagag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1012

<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1012
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu

370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Arg Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1013
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1013
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatttctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgccgtgg agattgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
accattagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 1014
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1014
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430

Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1015
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1015
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatttctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1016
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1016
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45

Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1017

<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1017
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg agattgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
accattagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1018
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1018
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys

100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1019
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1019
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1020
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1020
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160

Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1021
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1021
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360

ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg aggttgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1022
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1022
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser

210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Val Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1023
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1023
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780

gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatttctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1024
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1024
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270

Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1025
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1025
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200

accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1026
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1026
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro

325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1027
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1027
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcggccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgcaaatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatttg 660
accgaactga gcaatgtcaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 1028
<211> 451

<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1028
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380

Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1029
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1029
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg aggttgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1030
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1030

Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Val Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn

435 440 445
Lys Tyr Lys
450

<210> 1031
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1031
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatgcact gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc accgggcaat 600
ggtcaaatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1032
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1032
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr

50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ala Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1033
<211> 1353

<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1033
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatttctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1034
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1034
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110

Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1035
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1035

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tggcttgcgg agggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc accgggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtcaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgta 780
gtctatgtga gctttggcag cgaatatttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1036
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1036
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys

165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1037
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1037
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420

ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc accgggcaat 600
ggtcaaatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaatgtcaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1038
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1038
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220

Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1039
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1039
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtggcg 840

ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg aggttgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accgttaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1040
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1040
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val

275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Val Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Val Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1041
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1041
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc accgggcaat 600
ggtcaaatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260

attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1042
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1042
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335

Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1043
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1043
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattgccac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaatgtcaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1044
<211> 451
<212> PRT

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1044
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Ala Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu

385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1045
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1045
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1046
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1046
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val

1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445

Lys Tyr Lys
450

<210> 1047
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1047
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
ggtggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatatttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1048
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1048
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60

Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1049
<211> 1353
<212> DNA

<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1049
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg agattgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1050
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1050
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln

115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1051
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1051
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60

tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc accgggcaat 600
ggtcaaatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatttg 660
accgaactga gcaatgtcaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatatttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1052
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1052
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175

Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1053
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1053
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480

aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 1054
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1054
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr

225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1055
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1055
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgcaaatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgta 780
gtctatgtga gctttggcag cgaatatttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900

gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1056
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1056
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285

Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1057
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1057
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320

atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1058
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1058
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu

340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1059
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1059
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcctttctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1060
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1060
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Leu Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400

Thr Leu Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1061
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1061
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatatttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1062
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1062
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15

Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys

450

<210> 1063
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1063
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatttctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg agattgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accattagag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1064
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1064
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu

65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Arg Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1065
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1065
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaatgtcaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1066
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1066
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125

Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1067
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1067
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120

ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1068
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1068
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu

180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1069
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1069
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatgcact gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540

aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc accgggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatttg 660
accgaactga gcaatgtcaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgta 780
gtctatgtga gctttggcag cgaatctttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1070
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1070
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ala Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240

Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1071
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1071
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc accgggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatttg 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatctttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960

cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1072
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1072
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Ser Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu

290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1073
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1073
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatttctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgccgtgg agattgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accgttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1074
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1074
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350

Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Val Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1075
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1075
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcggccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1076
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1076
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly

405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1077
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1077
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcgttat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttacc ggaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttggcgtgg agattgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accgttagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1078
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 954

<400> 1078
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn

20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Val Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Pro Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Val Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1079
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1079
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1080
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1080
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1081

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1081
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgttg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1082
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1082
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1083
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1083
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccaag ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1084
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1084
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Gln Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1085
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1085
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtctccg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1086
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1086
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Ser Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1087
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1087
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gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tcctgcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgacgta ccgatggag 2379

<210> 1088
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1088
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Leu Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asp Val Pro Met Glu
785 790

<210> 1089
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1089
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gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctaca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1090
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1090
Met Ile Glu Ala Leu Arg Thr Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1091
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1091
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gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaatatccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1092
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1092
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu

85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Tyr Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1093
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1093
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tcgagcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1094
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1094
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Glu Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1095
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1095
atgattgaag aactgcgcca acagacactg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgctgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgttg gtgccgagaa tgtgcacatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1096
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1096
Met Ile Glu Glu Leu Arg Gln Gln Thr Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val His Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1097
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1097
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct gccggaaggc tatgctgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtttctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1098
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1098
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160

Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1099
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1099
atgattgaag aactgcgcca acagctgctg gatgatcggc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccaag ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgttg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140

caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtttctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1100
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1100
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Arg Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Gln Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1101
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1101
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
catcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320

gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1102
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1102
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg His Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1103
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1103
atgattgaag aactgcgcca acagctgctg gatgatcggc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccaag ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1104
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1104
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Arg Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Gln Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1105
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1105
atgattgaag aactgcgcca acagctgctg gatgatcggc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1106
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1106
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Arg Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1107
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1107
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggatttta aggaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1108
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1108
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Lys Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1109
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1109
atgattgaag aactgcgcca acagctgctg gatgatcggc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccaag ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgttg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1110
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1110
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Arg Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Gln Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1111
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1111
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccaag ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agatccgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgttg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtttctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1112
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1112
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Gln Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1113
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1113
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cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcctgagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1114
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1114
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Leu Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1115
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1115
atgattgaag cactgcgcca aatgctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1116

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1116
Met Ile Glu Ala Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1117
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1117
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttaga tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggact 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1118
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1118
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Asp Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Thr Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1119
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1119
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
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gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1120
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1120
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Thr Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1121
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1121
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cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1122
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1122
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1123
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1123

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cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cacggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1124
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1124
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Thr Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1125
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1125
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180

tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa gtggaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1126
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1126
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Val Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1127
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1127
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360

gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tcactcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1128
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1128
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Thr Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1129
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1129
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aaagtctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540

ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1130
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1130
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1131
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1131
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgcggctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1132
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1132
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Arg Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1133
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1133
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaaa aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagtacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1134
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1134
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe

145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Lys Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1135
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1135
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080

cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcct 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1136
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1136
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1137
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1137
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1138
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1138
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1139
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1139
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tctgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1140
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1140
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Cys Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1141
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1141
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgactctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1142
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1142
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Thr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1143
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1143
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaaa ctgaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1144
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1144
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1145
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1145
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1146
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1146
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1147
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1147
atgattgaag cactgcgcca acagctgctg gatgatccac gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1148
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1148
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1149
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1149
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cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tcgtgcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1150
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1150
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Val Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1151
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1151
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cgtcatttag tcgcatctca gcgtgactca tggttatata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct gccggaaggc tatgcagaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
gcgcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgtag gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgttcctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1152
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 74

<400> 1152
Met Ile Glu Ala Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Tyr Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Ala Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Ala Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Val Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Phe Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1153
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1153
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaaa ccgaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cacagagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgagca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1154
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1154
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Thr Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Ser Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1155
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1155
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatagag aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcatacacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgttga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgattcgaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tggttatcgg tggtcatatt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1156
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1156
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Val Ile Gly Gly His Ile Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1157
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1157
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gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1158
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1158

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1159
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1159
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1160
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1160
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1161
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1161
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatgg ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccacgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtaccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatt 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1162
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1162
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45

Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Val Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Thr Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1163
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1163
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300

ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tctgcgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaagattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1164
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1164
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1165
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1165
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtctggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480

agcgatttag cagcaggtcg tagtcagctt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1166
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1166
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95

Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Leu Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1167
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1167
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660

cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggagg 1320
gatcatgaaa ccgaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgagca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcacgccgta ccgtcggag 2379

<210> 1168
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1168
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Ser Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Ser Glu
785 790

<210> 1169
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1169
atgattgaag aactgcgcca gcagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggatttta gagaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
catcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccacg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacggccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1170
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1170
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg His Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1171
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1171
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggga gtatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcgac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagact ttatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg ggcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gctctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc ggccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1172
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1172
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asp Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Phe
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Ala Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1173
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1173
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgagcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaaa ccgaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgatggag 2379

<210> 1174
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1174
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1175
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1175
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cacagagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1176
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1176
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Thr Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1177
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1177
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tctgcgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaagattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560

tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1178
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1178
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1179
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1179
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggacg 1320
gatcatgaaa ccgaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgatggag 2379

<210> 1180
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1180
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Thr Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1181
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1181
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggacg 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920

gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcacgccgta ccgatggag 2379

<210> 1182
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1182
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Thr Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1183
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1183
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagcgaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgg 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgctgaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggattatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca agctctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggcggaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatccctacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt tgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1184
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1184
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Leu Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Tyr Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1185
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1185
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaaa ccgaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgtcggag 2379

<210> 1186
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1186
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala Glu Ala Val Pro Ser Glu
785 790

<210> 1187
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1187
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttt cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cgtggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaac accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccggac ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct tcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1188
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1188
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1189
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1189
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggacg 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgagt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgtcggag 2379

<210> 1190
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1190
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Thr Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Ser Glu
785 790

<210> 1191

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1191
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
gaatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgatggag 2379

<210> 1192
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1192
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Glu Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1193
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1193
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatgtgg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcatacacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaataa gcgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgattatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1194
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1194
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Lys Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1195
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1195
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtaccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaagc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggccacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatt 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gttggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacgggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1196
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1196
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Thr Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Arg Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1197
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1197
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgcctg tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatt 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1198
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1198
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro

35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Leu Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1199
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1199
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240

ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtaccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggccacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgcctg tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gttggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1200
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1200
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Thr Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Leu Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1201
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1201
atgattgaag aactgcgcca gatgctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
catcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1202
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1202
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu

85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg His Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1203
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1203
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcaccgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcattac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaacggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcttaga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1204
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1204
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1205
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1205
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggagg 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgatggag 2379

<210> 1206
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1206
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1207
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1207
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagcgaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcggaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcacagct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcat tgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1208
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1208
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160

Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Ile Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1209
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1209
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatgtgg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcatacacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgttga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140

caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatccgaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcat cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tggttatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcatgccgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1210
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1210
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp His Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Val Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Cys Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1211
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1211
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gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgacgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caaccgtaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcctacacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatattga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320

gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaataa gcgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcatgccgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1212
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1212
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Arg Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Leu
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Ile Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Lys Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Cys Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1213
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1213
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacgctgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtc tggatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga aaggtatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgttac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagcacggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagaacgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtgaactg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagttgcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgggtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1214
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1214
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Leu Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Leu Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu His Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Glu Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Glu Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Gly Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1215
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1215
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggagg 1320
gatcatgaaa ccgaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgatggag 2379

<210> 1216
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1216
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1217
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1217
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gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aactcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgtggagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaagccgta ccgatggag 2379

<210> 1218
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1218
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Leu Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1219
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1219
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcatcg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtaacgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggtaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgcaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagccgcat cctgatcgtg agcatacacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaaat tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacgcttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcatgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatccgaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcat cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgattatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtggcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgacaatcg cgcgtatttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1220
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1080

<400> 1220
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asn Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Ala Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Arg Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Ile Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp His Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1221
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1221
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1222
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1222
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1223
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1223
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1224
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1224
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1225
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1225
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcggaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1226

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1226
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1227
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1227
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1228
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1228
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1229
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1229
atgattgaag aactgcgcca acaactgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatgttg aacagctggc cgtggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aagaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc acccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcacgccgta ccgatggag 2379

<210> 1230
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1230
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1231
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1231
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcggaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1232
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1232
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1233
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1233

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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagctt ctggaatttc tgagcctgca tcgtctggat 540
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cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1234
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1234
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Leu Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1235
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1235
atgattgaag aactgcgcca aatgctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180

tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcctgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgttgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1236
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1236
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1237
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1237
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360

gaagcagttc tgacggtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
gaatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcgac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcggaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1238
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1238
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Glu Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asp Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1239
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1239
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagctt ctggaatttc tgagcctgca tcgtctggat 540

ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1240
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1240
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Leu Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1241
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1241
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatgg ttagcaacat tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcggaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1242
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1242
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Val Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1243
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1243
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagctt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcgac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctacaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1244
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1244
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe

145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Leu Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asp Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1245
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1245
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatgg ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaagattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1246
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1246
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Val Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1247
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1247
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagctt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1248
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1248
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Leu Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1249
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1249
atgattgaag aactgcgcca aatgctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aatcactggc cgtggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcctgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aagaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgttgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc acccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgattatcgg tggtcatatt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1250
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1250
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Ile Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1251
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1251
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cgtggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
catcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcctgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aagaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaataa gagagagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc acccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tggttatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1252
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1252
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg His Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Asp Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Lys Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Val Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1253
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1253
atgattgaag aactgcgcca aatgctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aatcactggc cgtggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cacagagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tggttatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcacgccgta ccgagcgag 2379

<210> 1254
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1254
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Thr Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Val Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Ser Glu
785 790

<210> 1255
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1255
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gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaaa ctgaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1256
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1256
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1257
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1257
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcgttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgctgaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1258
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1258
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Leu Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1259
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1259
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagctt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatgg ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca ttatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1260
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1260
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Leu Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Val Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1261
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1261
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatgg ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc ggccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1262
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1262
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Val Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Ala Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1263
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1263
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatgttg aatcactggc cgtggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
catcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcctgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tggttatcgg tggtcatatt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1264
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1264
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Ser Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg His Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Val Ile Gly Gly His Ile Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1265
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1265
atgattgaag aactgcgcca acaactgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatgttg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggacg 1320
gatcatgaaa ctgaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cgttgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc acccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tggttatcgg tggtcatgtt 1800
gatgtgagca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1266
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1266
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Thr Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Val Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Val Ile Gly Gly His Val Asp Val Ser Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1267
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1267
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcggaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc ggccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1268
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1268

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Ala Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1269
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1269
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1270
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1270
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1271
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1271
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca ttatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1272
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1272
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45

Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1273
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1273
atgattgaag aactgcgcca acaactgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatgttg aatcactggc cctggaggag 300

ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaaa ctgaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1274
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1274
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Thr Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1275
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1275
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480

agcgatttag cagcaggtcg tagtcagctt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1276
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1276
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95

Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Leu Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1277
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1277
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gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatgttg aatcactggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggcattg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcctgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggacg 1320
gatcatgaac aagaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tggttatcgg tggtcatatt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1278
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1278
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Ser Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Ile Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Thr Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Val Ile Gly Gly His Ile Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1279
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1279
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt gggtggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1280
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1280
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Val Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1281
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1281
atgattgaag aactgcgcca acaactgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatgttg aatcactggc cgtggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcctgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aagaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc acccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcacgccgta ccgagcgag 2379

<210> 1282
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1282
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Val Glu Ser Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Ser Glu
785 790

<210> 1283
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1283
atgattgaag aactgcgcca aatgctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatctt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tgaggccgta ccgatggag 2379

<210> 1284
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1284
Met Ile Glu Glu Leu Arg Gln Met Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Glu Ala Val Pro Met Glu
785 790

<210> 1285
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1285
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtaggtggat ttatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttcgaggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatc ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agattcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgta gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1286
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1286
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Arg Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Ile Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1287
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1287
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggat atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgcctatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttcagggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
cagtatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat cctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcggaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtaccttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaagattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560

tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtatttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1288
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose Synthase Variant of SEQ ID NO: 1158

<400> 1288
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Ile Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Ala Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Arg Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Ile Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1289
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 1289
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta tcattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gattctgcaa ctggcgaacg tgctgtacag caagggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt tcatcttgga caacgatccg caggacgagc gtattagcaa cctgccgacc 240
catggtccgc tggcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaactg 300
cgtcgtgagc tggaactgct gatgctggcg agcgaggaag acgaggaagt tagctgcctg 360
attaccgatg cgctgtggta cttcgcgcaa agcgtggcgg acagcctgaa cctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc acgtgagcct gccgcagttt 480
gacgagcttg gctacctgga tccggacgat aaaacccgtc tggaggaaca agcgagcggt 540
ttcccgatgc tgaaggttaa agatatcaag agcgcgtata gcaactggca gatcctgaaa 600
gaaattctgg gcaagatgat caagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatcc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgacc gcgagcagca gcagcctgct ggaccacgat 780
cgtaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcgc gaacgcgatt cgtcgtgtga tggttgacga ggaaggtgag 1260
tacatccgtc agaacgcgcg tgttctgaag caaaaagcgg atgttagcct gatgaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 1290
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 32

<400> 1290
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Ile Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu
100 105 110
Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln Phe
145 150 155 160
Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys
420 425 430
Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 1291
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 1291
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccggtt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1292
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 1292
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15

Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys

450

<210> 1293
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 1293
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgt atggtcatat ttctccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatttt gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgatattct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg aacgaagaag atcgcttagc agaacataat 600
atgcagatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacatgga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctttgtgt gctttggcag cgagtacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg acaagtttgc accgcagcca cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagcc ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcacaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaga acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 1294
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> ADP-Glycosyltransferase Variant of SEQ ID NO: 770

<400> 1294
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Tyr Gly His Ile Ser Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Phe Val Glu Leu His Leu Pro Glu Leu Pro Glu

65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Ile Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asn Glu
180 185 190
Glu Asp Arg Leu Ala Glu His Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Phe Val Cys Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp Lys Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Leu Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 1295
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1295
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1296
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1296
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1297
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1297
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1298
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1298
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1299
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1299
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1300
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1300
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro

35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1301
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1301
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tagatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1302
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1302
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1303
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1303
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgcg aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcagtggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1304
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1304
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu Gln Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1305
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1305
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1306
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1306
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1307
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1307
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccgtcc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1308
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1308
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1309
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1309
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1310
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1310
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160

Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1311
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1311
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140

caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1312
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1312
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1313
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1313
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320

gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1314
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1314
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1315
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1315
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1316
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1316
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1317
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1317
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1318
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1318
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1319
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1319
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1320
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1320
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1321
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1321
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgcg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1322
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1322
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1323
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1323
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1324
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1324
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1325
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1325
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgcttct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1326
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1326
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1327
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1327
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1328

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1328
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1329
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1329
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgcg aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1330
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1330
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1331
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1331
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1332
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1332
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1333
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1333
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1334
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1334
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1335
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1335

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1336
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1336
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1337
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1337
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1338
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1338
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1339
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1339
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360

gaagcagttc tggaagtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1340
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1340
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1341
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1341
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tggaagtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1342
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1342
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Glu Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1343
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1343
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1344
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1344
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1345
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1345
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1346
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1346
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe

145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1347
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1347
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080

cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1348
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1348
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1349
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1349
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atgggacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1350
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1350
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Gly Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1351
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1351
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1352
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1352
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1353
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1353
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1354
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1354
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Asp Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1355
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1355
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1356
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1356
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1357
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1357
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1358
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1358
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1359
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1359
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1360
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1360
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1361
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1361
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1362
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1362
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1363
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1363
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1364
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1364
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1365
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1365
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgcg aacagctggc cgtggaggag 300
ctgagcactg atgaatatct acaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1366
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1366
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1367
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1367
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1368
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1368
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1369
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1369
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcaga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1370
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1370

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Gln Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1371
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1371
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1372
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1372
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1373
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1373
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1374
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1374
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45

Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1375
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1375
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1376
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1376
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1377
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1377
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480

agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1378
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1378
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ala Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1379
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1379
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccagatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtggcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1380
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1380
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Trp Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1381
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1381
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgcgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1382
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1382
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1383
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1383
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgcg aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctcgccgtcc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctggaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1384
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1384
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Glu Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1385
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1385
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgtg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1386
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1386
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1387
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1387
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aagatttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgc 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1388
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1388
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Ile Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1389
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1389
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagca tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatcgcg aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga cgcgccggat ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tcccgatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggcgg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560

tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccga aatattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1390
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1390
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln His Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Arg Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ala Pro Asp Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1391
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1391
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1392
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1392
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1393
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1393
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc agttagcagg ccgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1394
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1394
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Gln Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1395
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1395
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt gctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg taatgaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaacga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagaca acgttagcgg cttccatatt 2100

gatcccaacg accatgaagc gaccgcagaa cggctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga agaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1396
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1396
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Val Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Glu Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Asn Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1397
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1397
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt gctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg taatgaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gaaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa tcgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gataacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaacga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accatgaagc gaccgcagaa cggctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga agaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1398
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1398
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Val Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp Asn Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Asn Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1399
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1399
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgctttgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1400
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1400
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1401
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1401
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcacccttcc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgctttgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1402
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1402
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1403

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1403
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcaa ggaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacatat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1404
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1404
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Lys Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1405
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1405
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcacccttcc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcaa ggaggatggt 1080
cgtattcacc ggcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacatat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgctttgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1406
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1406
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Lys Glu Asp Gly Arg Ile His Arg His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1407
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1407
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc ggccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagaccc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1408
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1408
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1409
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1409
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1410
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1410
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1411
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1411
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1412
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1412
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Asp Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1413
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1413
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1414
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1414
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1415
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1415
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1416
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1416
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1417
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1417
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1418
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1418
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1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1419
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1419
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1420
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1420
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160

Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1421
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1421
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
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gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
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agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1422
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1422
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1423
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1423
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320

gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1424
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1424
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1425
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1425
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1426
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1426
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1427
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1427
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1428
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1428
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1429
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1429
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1430
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1430
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1431
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1431
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1432
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1432
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1433
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1433
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1434
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1434
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1435
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1435
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1436
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1436
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1437
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1437
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1438

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1438
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1439
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1439
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1440
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1440
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1441
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1441
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagact tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1442
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1442
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Phe
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1443
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1443
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1444
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1444
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1445
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1445

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1446
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1446
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1447
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1447
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180

tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1448
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1448
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1449
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1449
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360

gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1450
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1450
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1451
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1451
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1452
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1452
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1453
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1453
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1454
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1454
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1455
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1455
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1456
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1456
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe

145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1457
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1457
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1458
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1458
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1459
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1459
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1460
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1460
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1461
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1461
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1462
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1462
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1463
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1463
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1464
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1464
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1465
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1465
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
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gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
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agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
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gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1466
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1466
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1467
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1467
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1468
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1468
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1469
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1469
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1470
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1470
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1471
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1471
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1472
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1472
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1473
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1473
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1474
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1474
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1475
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1475
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgcatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1476
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1476
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu His Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1477
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1477
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1478
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1478
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1479
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1479
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1480
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1480

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1481
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1481
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1482
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1482
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1483
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1483
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1484
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1484
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1485
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1485
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1486
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1486
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1487
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1487
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480

agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1488
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1488
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1489
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1489
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1490
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1490
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1491
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1491
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1492
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1492
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1493
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1493
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat ttttgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1494
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1494
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Cys Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1495
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1495
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1496
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1496
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1497
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1497
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1498
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1498
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1499
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1499
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcagtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560

tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1500
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1500
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ser Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1501
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1501
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1502
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1502
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1503
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1503
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgccg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgc atccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1504
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1504
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu His Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1505
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1505
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatctgg 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1506
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1506
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Trp
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1507
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1507
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1508
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1508
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1509
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1509
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
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gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcatg 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
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caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1510
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1510
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Met
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1511
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1511
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagagctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1512
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1512
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Glu Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1513

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1513
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgggc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1514
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1514
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Gly Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1515
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1515
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcgag 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1516
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1516
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Glu
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1517
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1517
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcgct 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1518
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1518
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Ala
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1519
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1519
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
agtgatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1520
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1520
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1521
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1521
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1522
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1522
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1523
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1523
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcgcgtat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1524
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1524
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Ala Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1525
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1525
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcgatctggc tcatgccgta ccgatggag 2379

<210> 1526
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1526
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Asp Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1527
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1527
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gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtga gagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1528
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1528
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1529
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1529
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1530
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1530
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160

Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Val Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1531
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1531
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagatctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1532
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1532
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Asp Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1533
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1533
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtgcggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320

gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1534
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1534
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Ala Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1535
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1535
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1536
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1536
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1537
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1537
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1538
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1538
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1539
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1539
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1540
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1540
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1541
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1541
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gaaggctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1542
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1542
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Arg Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1543
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1543
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcgggtat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1544
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1544
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Gly Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1545
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1545
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagc gcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1546
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1546
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Ala Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1547
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1547
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagaggttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1548

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1548
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1549
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1549
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1550
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1550
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ala Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1551
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1551
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1552
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1552
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1553
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1553
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagattct cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1554
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1554
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ser Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1555
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1555

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctactc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1556
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1556
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Thr Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1557
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1557
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180

tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatctct 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1558
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1558
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Ser
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1559
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1559
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360

gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcaat 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1560
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1560
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Asn
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1561
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1561
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgctcgtat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1562
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1562
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Ser Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1563
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1563
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcatt tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1564
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1564
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Phe Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1565
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1565
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agtgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cctggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttccgagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc gtttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgttc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1566
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1566
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Val Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Arg Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Phe

145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Val Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ala Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1567
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1567
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctata cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1568
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1568
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Thr Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1569
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1569
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctata cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc atggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1570
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1570
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Thr Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1571
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1571
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccggcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1572
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1572
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1573
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1573
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcccgcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccgcaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tgcagatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc atggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1574
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1574
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Val Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Pro Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Gln Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1575
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1575
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccggcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctata cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc atggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1576
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1576
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Val Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Thr Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1577
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1577
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccggcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctata cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcacga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1578
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1578
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Thr Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp His Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1579
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1579
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccgcaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttttat 1560
tttagctatg cacgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc atggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1580
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1580
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Gln Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1581
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1581
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1582
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1582
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1583
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1583
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1584
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1584
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1585
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1585
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gataacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1586
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1586
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Val Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp Asn Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1587
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1587
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcccgcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gataacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1588
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1588
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Pro Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp Asn Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1589
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1589
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccgcaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctata cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcgt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc atggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1590
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1590

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Val Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Gln Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Thr Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1591
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1591
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccggcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctata cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1592
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1592
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Thr Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1593
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1593
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gataacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
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ctgtttggcc gcgaaccagg tgcagatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc atggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgc 2160
aaacgtccgc actattggct tgaaattagc gatgcggctc ttgcgcgcgt cgcagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1594
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1594
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp Asn Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Thr Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Lys Arg Pro His Tyr Trp Leu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1595
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1595
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc cgtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggccttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccggcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt actccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttctat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1596
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1596
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Phe Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ala Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1597
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1597
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggta tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag gtattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagcccgcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480

agcgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcatgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1598
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1598
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Tyr Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Gly Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Val Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Pro Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Ser Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Ala Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1599
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1599
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ttcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1600
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1600
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1601
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1601
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcctg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ttcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtataccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatttt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcatg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1602
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1602
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Leu Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Tyr Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Phe Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Met Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1603
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1603
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ttcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcatg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1604
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1604
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Met Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1605
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1605
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcctg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattgggt ttcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtataccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggtc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaacaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatttt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcatg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1606
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1606
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Leu Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Val Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Tyr Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Gln Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Phe Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Met Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1607
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1607
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcctg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ttcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcat atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1608
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1608
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Leu Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp His Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1609
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1609
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1610
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1610
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1611
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1611
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcctg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttggttgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1612
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1612
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Leu Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Val Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1613
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1613
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgt atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1614
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1614
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1615
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1615
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaaac 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1616
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1616
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Asn
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1617
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1617
atgattgaag aactgcgcca acagctgctg gatgatccga ggtcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtctgggtt ttgaaccagg ttggggcaac accgcgggcc gtgttagcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgcggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcggtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1618
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1618
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Leu Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Ser Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1619
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1619
atgattgaag aactgcgcca acagctgctg gatgatccgg actcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtaa attacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcatta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgt atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agctgtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1620
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1620
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Asp Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Lys Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe His Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Leu Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1621
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1621
atgattgaag aactgcgcca acagctgctg gatgatccgg actcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcat atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agctgtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1622
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1622
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Asp Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp His Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Leu Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1623

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1623
atgattgaag aactgcgcca acagctgctg gatgatccga ggtcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcggggtt ttgaaccagg ttggggcaac accgcgggcc gtgttagcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1624
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1624
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Ser Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1625
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1625
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtag attacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgagaatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcatta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcat atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcggtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1626
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1626
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe His Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp His Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1627
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1627
atgattgaag aactgcgcca acagctgctg gatgatccga ggtcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtag attacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tacgatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtctgggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcatta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcggtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1628
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1628
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Thr Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Leu Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe His Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1629
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1629
atgattgaag aactgcgcca acagctgctg gatgatccgg actcatggga tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtag attacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcat atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcggtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1630
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1630
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Asp Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp His Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1631
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1631
atgattgaag aactgcgcca acagctgctg gatgatccga ggtcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtaa attacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgaaaatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcggctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcat atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcggtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1632
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1632
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Lys Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Lys Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp His Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1633
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1633
atgattgaag aactgcgcca acagctgctg gatgatccga ggtcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtag attacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcggggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgaaaatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcggctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcatta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgt atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgcggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtagcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcggtatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1634
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1634
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Lys Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe His Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Ser Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1635
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1635
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcagagca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgtatcttt 480
accgatttag aagaaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggaag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggaacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcactggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctgaatt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc aaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1636
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1636
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Glu Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Glu Glu Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Glu Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Glu Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1637
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1637
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaagtca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttaga agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgaagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1638
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1638
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Glu Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Glu
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1639
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1639
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaagtca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgtatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggaag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cggaatggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatga gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgttt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaaga aaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1640
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1640
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Glu Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro Glu Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Glu Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Glu Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1641
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1641
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaagtca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttaga agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tgaaatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggaag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatgaaacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcactggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgaagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1642
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1642
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Glu Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Glu Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Glu Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Glu Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Glu
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1643
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1643
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcagagca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttaga agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgtatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggaacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cggaatggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1644
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1644
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Glu Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Glu Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro Glu Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1645
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1645
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaagtca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttaga agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgtatcttt 480
accgatttag aagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggaacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcactggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaaga aaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1646
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1646
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Glu Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Glu Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Glu Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1647
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1647
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaagtca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgtatcttt 480
accgatttag cagaaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc gaacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggaacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcactggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgttt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc aaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1648
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1648
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Glu Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Glu Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1649
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1649
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaagtca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttaga agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgtatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc gaacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatgaaacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgttt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc aaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1650
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1650
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Glu Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Glu Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Glu Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1651
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1651
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaagtca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttaga agcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgtatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggaag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cggaatggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggcca 1320
gaccacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatga gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgttt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc aaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1652
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1652
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Glu Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Glu Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro Glu Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Glu Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1653
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1653
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgggc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1654
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1654
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Gly Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1655
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1655
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctggtgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1656
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1656
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Val Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1657
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1657
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctacgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gaagtctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1658

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1658
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Thr Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1659
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1659
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgtgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcggttat 1560
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1660
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1660
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Val Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Gly Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1661
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1661
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgtgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1662
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1662
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Val Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1663
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1663
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctacgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctggtgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1664
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1664
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Thr Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Val Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1665
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1665

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctacgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagaactgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1666
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1666
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Thr Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Glu Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1667
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1667
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctacgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct agagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacttat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctggtgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1668
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1668
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Thr Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Val Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Arg Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1669
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1669
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagc tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctacgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1670
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1670
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Ala Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Thr Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1671
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1671
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctacgc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcttgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gagacctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggccc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1672
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1672
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Thr Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Leu Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Asp Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1673
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1673
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1674
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1674
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1675
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1675
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
actgatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1676
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1676
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe

145 150 155 160
Thr Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1677
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1677
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1678
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1678
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1679
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1679
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatt 480
accgatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
catgatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1680
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1680
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Ile
145 150 155 160
Thr Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala His Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1681
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1681
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1682
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1682
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ser Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1683
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1683
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1684
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1684
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1685
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1685
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
actgatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1686
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1686
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1687
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1687
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1688
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1688
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1689
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1689
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1690
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1690
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1691
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1691
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1692
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1692
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1693
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1693
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1694
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1694
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1695
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1695
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1696
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1696
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1697
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1697
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1698
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1698
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1699
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1699
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1700
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1700

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1701
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1701
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1702
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1702
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1703
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1703
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1704
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1704
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1705
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1705
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
actgatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1706
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1706
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1707
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1707
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480

accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1708
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1708
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1709
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1709
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1710
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1710
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1711
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1711
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1712
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1712
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ser Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1713
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1713
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1714
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1714
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ser Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1715
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1715
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1716
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1716
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1717
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1717
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1718
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1718
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1719
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1719
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560

tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1720
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1720
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1721
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1721
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaaa 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1722
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1722
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1723
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1723
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1724
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1724
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1725
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1725
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1726
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1726
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1727
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1727
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1728
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1728
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1729
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1729
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1730
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1730
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1731
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1731
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1732
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1732
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1733

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1733
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1734
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1734
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1735
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1735
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1736
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1736
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Gln Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1737
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1737
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1738
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1738
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1739
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1739
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1740
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1740
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Gln Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ser Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1741
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1741
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1742
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1742
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1743
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1743
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgtgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1744
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1744
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Val Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1745
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1745
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtga aagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1746
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1746
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Glu Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1747
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1747
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1748
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1748
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1749
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1749
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1750
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1750
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ser Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1751
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1751
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1752
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1752
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1753
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1753
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1754
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1754
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1755
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1755
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1756
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1756
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1757
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1757
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
caggatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1758
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1758
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Gln Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1759
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1759
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1760
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1760
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1761
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1761
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accataaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1762
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1762
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Lys Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1763
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1763
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1764
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1764
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1765
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1765
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagcagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatatg cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1766
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1766
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Met Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1767
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1767
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagaagttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcttt 480
accgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatagc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1768

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1768
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Glu Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Phe
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Ser Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1769
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1769
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1770
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1770
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1771
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1771
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatcatg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttatgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
caggatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagataga cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgctgct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1772
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1772
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Met
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Met Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Gln Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Arg Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Leu Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1773
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1773
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccattgat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1774
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1774
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1775
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1775

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1776
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1776
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1777
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1777
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaaatg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1778
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1778
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Met Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1779
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1779
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttctttatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1780
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1780
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe Phe Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1781
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1781
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtatctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1782
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1782
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1783
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1783
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg acatggaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1784
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1784
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Met Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1785
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1785
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1786
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1786
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1787
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1787
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg agcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1788
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1788
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1789
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1789
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg agcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttttggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatat cgttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcat atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1790
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1790
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Ile Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp His Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1791
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1791
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg agcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcctg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttttggatca ggcccgagca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct cgttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1792
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1792
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Leu Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1793
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1793
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttaga agcagaaggt 360
gaagatgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcctg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct cgttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtatg 1620

ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1794
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1794
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Glu Ala Glu Gly Glu Asp Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Leu Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Met Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1795
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1795
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgagca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatac tgttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1796
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1796
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Thr Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1797
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1797
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggacagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg acatggaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1798
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1798
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Met Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1799
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1799
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggacagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaaatg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1800
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1800
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Met Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1801
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1801
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1802
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1802
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1803
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1803
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1804
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1804
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1805
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1805
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtgatcc atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggacagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1806
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1806
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ile His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1807
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1807
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1808
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1808
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1809
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1809
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagagat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaaatg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1810
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1810

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Met Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1811
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1811
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggacagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttctttatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1812
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1812
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe Phe Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1813
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1813
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa cgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg acatggaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1814
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1814
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Met Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1815
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1815
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1816
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1816
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1817
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1817
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1818
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1818
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1819
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1819
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
ggtcagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccacttat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tgcagatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accatgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1820
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1820
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Gly Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Ala Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
His Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1821
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1821
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1822
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1822
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1823
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1823
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtatctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaaac 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttcttcatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1824
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1824
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Asn
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe Phe Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1825
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1825
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1826
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1826
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1827
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1827
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaaac 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1828
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1828
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Asn
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1829
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1829
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1830
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1830
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1831
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1831
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccacatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1832
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1832
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1833
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1833
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcactggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccactaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaaatg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccacatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1834
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1834
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Met Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1835
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1835
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1836
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1836
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Met Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1837
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1837
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccactaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1838
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1838
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1839
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1839
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1840
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1840
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1841
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1841
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtatctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccacatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1842
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1842
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1843

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1843
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa cgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtatctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccacatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1844
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1844
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1845
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1845
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtatctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaaac 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccacatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1846
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1846
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Asn
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1847
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1847
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccacatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1848
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1848
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1849
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1849
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg agtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatc cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccacatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1850
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1850
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1851
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1851
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctgggggaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1852
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1852
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Gly Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1853
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1853
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaagcgctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1854
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1854
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ala Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1855
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1855
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacaagt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1856
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1856
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Lys Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1857
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1857
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1858
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1858
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1859
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1859
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggct ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1860
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1860
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Leu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1861
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1861
atgattgaag aactgcgcca acagctgctg gatgataagc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1862
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1862
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Lys Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1863
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1863
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggctcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1864
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1864
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ala Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1865
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1865
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttacg gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1866
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1866
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Arg Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1867
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1867
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcat attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1868
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1868
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val His Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1869
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1869
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaactg 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1870
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1870
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Leu Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1871
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1871
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca acttctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1872
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1872
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Thr Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1873
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1873
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttagg gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1874
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1874
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gly Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1875
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1875
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaacggctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1876
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1876
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1877
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1877
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg ggcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1878

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1878
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1879
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1879
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1880
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1880
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Ser Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1881
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1881
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcatga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1882
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1882
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1883
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1883
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc gcttgaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1884
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1884
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Leu Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1885
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1885

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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1886
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1886
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1887
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1887
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggttg gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1888
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1888
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1889
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1889
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agcatgaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1890
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1890
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu His Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1891
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1891
atgattgaag aactgcgcca acagctgctg gatgatcatc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1892
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1892
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp His Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1893
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1893
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggaa ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1894
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1894
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Lys Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1895
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1895
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtcattggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1896
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1896
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly His Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1897
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1897
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtgctga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1898
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1898
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Ala Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1899
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1899
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatagggta ccgatggag 2379

<210> 1900
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1900
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Arg Val Pro Met Glu
785 790

<210> 1901
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1901
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataatgta ccgatggag 2379

<210> 1902
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1902
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 1903
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1903
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcggaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1904
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1904
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Gly Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1905
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1905
atgattgaag aactgcgcca acagctgctg gatgataatc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1906
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1906
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Asn Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1907
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1907
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aacatttagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1908
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1908
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu His Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1909
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1909
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca cggtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1910
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1910
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1911
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1911
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aagctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1912
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1912
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1913
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1913
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcagga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1914
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1914
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Gln Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1915
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1915
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtctgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1916
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1916
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Leu Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1917
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1917
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1918
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1918
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1919
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1919
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtattga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1920
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1920

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Ile Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1921
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1921
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gcggattttc gcgaacagct tccggaaggc tatccggaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1922
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1922
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1923
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1923
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagct tccggaaggc tattgggaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1924
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1924
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Trp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1925
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1925
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cgtcatttag tcgcatctca gcgtgaccat tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1926
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1926
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp His Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1927
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1927
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1928
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1928
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1929
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1929
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taatgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1930
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1930
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1931
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1931
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcaaaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1932
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1932
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Lys Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1933
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1933
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcggggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1934
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1934
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1935
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1935
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatagggaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1936
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1936
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Arg Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1937
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1937
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtgattgag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1938
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1938
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Ile Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1939
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1939
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgctgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560

tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1940
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1940
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Ala Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1941
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1941
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtaccctt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1942
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1942
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Pro Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1943
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1943
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc gacgcgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1944
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1944
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Thr Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1945
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1945
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttaa cggcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1946
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1946
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Thr Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1947
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1947
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagg gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1948
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1948
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Gly Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1949
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1949
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1950
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1950
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Arg Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1951
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1951
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tccggaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1952
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1952
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Pro
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1953

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1953
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tggtgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1954
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1954
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Gly Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1955
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1955
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg aggcggaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1956
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1956
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Ala Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1957
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1957
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgcct 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1958
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1958
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1959
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1959
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcaagggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1960
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1960
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Arg Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1961
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1961
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagcctc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1962
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1962
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Pro Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1963
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1963
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc ggggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1964
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1964
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gly Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1965
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1965
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtgtgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1966
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1966
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Val Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1967
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1967
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcacggat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1968
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1968
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1969
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1969
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttaa gtgcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1970
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1970
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ser Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1971
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1971
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt tagggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1972
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1972
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Arg Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1973
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1973
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgtggtggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1974
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1974
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro Trp Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1975
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1975
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggggaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1976
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1976
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1977
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1977
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgttcgctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1978
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1978
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1979
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1979
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt ctcggaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1980
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1980
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1981
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1981
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc acgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gtgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgagtcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1982
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1982
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1983
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1983
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1984
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1984
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ala Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Val Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1985
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1985
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1986
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1986
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 1987
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1987
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gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1988

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1988
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1989
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1989
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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<210> 1990
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1990
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1991
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1991
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gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1992
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1992
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1993
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 1993
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gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
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<210> 1994
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1994
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1995
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1995

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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaggctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1996
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1996
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1997
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1997
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 1998
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1998
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 1999
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 1999
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2000
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2000
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2001
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2001
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2002
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2002
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2003
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2003
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcatg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2004
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2004
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly His Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2005
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2005
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2006
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2006
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2007
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2007
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2008
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2008
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2009
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2009
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2010
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2010
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2011
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2011
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

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ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2012
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2012
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2013
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2013
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2014
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2014
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2015
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2015
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2016
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2016
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2017
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2017
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 2018
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2018
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2019
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2019
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2020
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2020
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2021
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2021
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2022
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2022
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Ala Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2023
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2023
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2024
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2024
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Thr Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2025
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2025
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2026
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2026
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20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2027
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2027
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2028
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2028
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2029
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2029
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2030
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2030

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2031
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2031
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tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2032
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2032
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2033
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2033
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2034
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2034
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2035
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2035
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2036
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2036
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2037
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2037
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2038
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2038
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2039
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2039
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2040
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2040
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2041
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2041
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2042
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2042
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2043
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2043
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gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag ctgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2044
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2044
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Ala Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2045
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2045
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2046
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2046
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2047
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2047
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2048
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2048
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2049
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2049
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
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gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

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ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2050
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2050
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2051
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2051
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2052
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2052
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2053
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2053
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atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2054
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2054
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2055
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2055
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2056
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2056
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2057
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2057
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2058
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2058
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2059
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2059
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2060
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2060
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2061
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2061
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2062
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2062
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2063

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2063
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2064
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2064
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2065
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2065
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2066
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2066
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2067
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2067
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2068
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2068
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2069
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2069
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2070
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2070
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2071
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2071
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2072
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2072
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2073
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2073
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gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2074
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2074
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2075
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2075
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2076
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2076
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2077
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2077
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2078
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2078
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2079
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2079
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2080
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2080
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2081
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2081
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2082
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2082
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2083
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2083
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2084
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2084
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2085
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2085
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2086
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2086
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2087
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2087
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2088
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2088
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2089
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2089
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2090
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2090
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2091
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2091
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2092
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2092
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2093
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2093
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gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
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gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2094
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2094
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2095
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2095
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gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2096
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2096
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 2097
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2097
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ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2098

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2098
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2099
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2099
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga cgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttt tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2100
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2100
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2101
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2101
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2102
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2102
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2103
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2103
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2104
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2104
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2105
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2105

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2106
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2106
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2107
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2107
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatggcgaag atattggtcc gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2108
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2108
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Gly Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2109
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2109
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggaccgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2110
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2110
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2111
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2111
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga cgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgacgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg taacgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tttagccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2112
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2112
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Asn Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2113
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2113
atgattgaag aactgcgcca acagctgctg gatgatccga agtcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2114
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2114
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Lys Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2115
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2115
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtg 1440
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2116
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2116
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1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2117
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2117
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgtata ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2118
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2118
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Tyr Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2119
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2119
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2120
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2120
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Val Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2121
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2121
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg cgttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2122
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2122
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2123
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2123
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatagg 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2124
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2124
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Arg Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2125
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2125
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaaaaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2126
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2126
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Lys Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2127
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2127
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcata atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2128
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2128
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val His Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2129
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2129
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcaatgat 180
tttgtggcac atacccagga agcgatcttc cgtaatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2130
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2130
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Asn Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asn Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2131
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2131
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2132
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2132
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Ser Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2133
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2133
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgc ctagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2134
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2134
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Pro Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2135
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2135
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
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actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2136
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2136
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Ile Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2137
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2137
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<210> 2138
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2138
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly His Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
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Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
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Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
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Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
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Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
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Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2139
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2139
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tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg cgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 2140
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2140

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Ala Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
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Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
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Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
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Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
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Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
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580 585 590
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595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2141
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

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<210> 2142
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2142
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Met Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2143
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2143
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcaca gtcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2144
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2144
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Ser His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2145
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2145
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc gttccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2146
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2146
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Arg Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2147
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2147
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtatgcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2148
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2148
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Tyr Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2149
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2149
atgattgaag aactgcgcca acagctgctg gatgatccgc gtatttggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2150
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2150
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ile Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2151
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2151
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatactga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2152
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2152
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Thr Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2153
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2153
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttt tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2154
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2154
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2155
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2155
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attggggtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2156
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2156
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile Gly Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2157
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2157
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tggggctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2158
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2158
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2159
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2159
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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<210> 2160
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2160
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Leu Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2161
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2161
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgc ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2162
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2162
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Arg Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2163
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2163
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tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
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gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2164
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2164
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Ser Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2165
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2165
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2166
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2166
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ile Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2167
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2167
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgta ggttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2168
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2168
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Arg Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2169
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2169
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atagttatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2170
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2170
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Ser Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2171
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2171
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctccgggat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2172
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2172
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Arg Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2173

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2173
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaatat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg ggaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2174
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2174
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Tyr Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2175
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2175
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtggggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2176
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2176
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Trp Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2177
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2177
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcagagca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2178
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2178
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Asp Ala Phe Leu Arg His Leu Val Ala Glu Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2179
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2179
atgattgaag aactgcgcca acagctgctg gatgatccgc gtccttggga tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2180
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2180
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Pro Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2181
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2181
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtatcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2182
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2182
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Tyr Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2183
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2183
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ttgcgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2184
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2184
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2185
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2185
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cactgggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2186
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2186
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Leu Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2187
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2187
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ggtcgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2188
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2188
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Gly Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2189
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2189
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtgagcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2190
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2190
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Glu His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2191
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2191
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggcta atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2192
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2192
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Ala Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2193
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2193
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2194
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2194
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2195
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2195
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2196
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2196
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Ser Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2197
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2197
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga aacgatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2198
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2198
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Thr Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2199
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2199
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agcgatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2200
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2200
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Ala Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2201
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2201
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcatg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2202
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2202
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Met Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2203
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2203
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgtctatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2204
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2204
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Ser Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2205
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2205
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2206
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2206
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ala Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 2207
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2207
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctctgggat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2208

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2208
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Trp Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2209
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2209
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctctcggat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2210
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2210
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Ser Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2211
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2211
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatacgcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2212
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2212
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Thr Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2213
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2213
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
actctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2214
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2214
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Thr Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2215
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2215

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga aaatatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2216
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2216
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asn Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2217
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2217
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg agttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2218
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2218
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Glu Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2219
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2219
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgg ggtccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2220
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2220
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Gly Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2221
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2221
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaagtgct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2222
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2222
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Val Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2223
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2223
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacgtct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2224
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2224
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Arg Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2225
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2225
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgcatcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2226
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2226
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1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala His Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2227
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2227
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2228
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2228
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Lys Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2229
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2229
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtt gtttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2230
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2230
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Cys Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2231
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2231
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2232
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2232
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Ser Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2233
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2233
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag caattggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
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atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2234
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2234
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ile Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2235
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2235
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2236
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2236
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Thr Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2237
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2237
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaga atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2238
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2238
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2239
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2239
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcggatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2240
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2240
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Arg Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2241
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2241
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagcct 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2242
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2242
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2243
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2243
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgt tgccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2244
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2244
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Leu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2245
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2245
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2246
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2246
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Gly Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2247
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2247
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctctgtgat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2248
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2248
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Cys Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2249
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2249
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggtgg agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2250
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2250

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Val Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2251
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2251
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2252
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2252
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Pro Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2253
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2253
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaaactct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2254
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2254
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Thr Leu Pro
35 40 45

Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2255
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2255
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctga agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2256
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2256
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Lys Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2257
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2257
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgcggat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2258
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2258
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2259
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2259
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaaattct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2260
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2260
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Ile Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2261
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2261
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gatggaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2262
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2262
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Met Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2263
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2263
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctga cgccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2264
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2264
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Thr Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2265
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2265
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaacgt tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2266
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2266
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Arg Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2267
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2267
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatcggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2268
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2268
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2269
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2269
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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<210> 2270
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2270
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Gly
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2271
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2271
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggt ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtt cgttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2272
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2272
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Val Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ser Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2273
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2273
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gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
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cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2274
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2274
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp His Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2275
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2275
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2276
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2276
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Ser Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2277
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2277
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatgag 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2278
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2278
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Glu Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2279
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2279
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt ccagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2280
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2280
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Gln Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2281
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2281
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatgat 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2282
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2282
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Asp Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2283

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2283
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgacgatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2284
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2284
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Thr Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2285
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2285
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgactctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2286
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2286
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Thr Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2287
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2287
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2288
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2288
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2289
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2289
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgtattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtgctcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2290
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2290
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Val Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ala His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2291
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2291
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtt ctttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2292
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2292
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ser Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2293
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2293
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcacta ctgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2294
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2294
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Thr Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2295
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2295
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcagcgca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2296
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2296
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ala Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2297
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2297
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaagggct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2298
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2298
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gly Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2299
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2299
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttactga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2300
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2300
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Leu Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2301
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2301
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga atcgatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2302
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2302
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Ser Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2303
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2303
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag caactggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2304
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2304
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Thr Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2305
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2305
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtggatatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2306
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2306
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Asp Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2307
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2307
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaaa tgattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2308
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2308
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Met Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2309
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2309
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcaactca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2310
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2310
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Thr Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2311
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2311
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cctgaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2312
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2312
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Leu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2313
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2313
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgcttctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2314
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2314
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Leu Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2315
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2315
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gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga acagatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2316
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2316
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Gln Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 2317
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2317
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggga tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatgatgaag atattggtcc gctcgtggat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt tctggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtggtctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cgaagaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tggatcgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2318

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2318
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Asp Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Asp Glu Asp Ile Gly Pro Leu Val Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Leu Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Gly Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Glu Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Asp Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2319
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2319
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2320
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2320
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2321
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2321
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2322
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2322
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2323
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2323
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt cttcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctatctgg agccattgat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgtga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2324
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2324
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Leu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2325
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2325

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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 2326
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2326
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2327
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2327
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2328
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2328
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2329
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2329
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgt attcatgtag aacagctggc ggtggaggag 300
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gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctctctgg agccattgat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2330
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2330
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2331
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2331
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2332
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2332
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2333
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2333
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctctctgg agccagagat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2334
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2334
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2335
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2335
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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<210> 2336
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2336
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2337
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2337
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2338
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2338
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Ala Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2339
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2339
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2340
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2340
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2341
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2341
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2342
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2342
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2343
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2343
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
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atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2344
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2344
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2345
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2345
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcat attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2346
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2346
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val His Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2347
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2347
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctatctgg agccattgat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcatga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2348
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2348
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Leu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2349
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2349
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcat attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcatga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2350
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2350
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val His Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2351
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2351
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctctctgg agccagagat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2352
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2352
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2353
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2353
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2354
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2354
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2355
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2355
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctctctgg agccagagat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgtga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2356
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2356
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2357
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2357
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctctctgg agccagagat cgaacgcctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2358
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2358
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2359
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2359
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccattgat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2360
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2360

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2361
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2361
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2362
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2362
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2363
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2363
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2364
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2364
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2365
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2365
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcat attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2366
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2366
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val His Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2367
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2367
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgtga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2368
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2368
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2369
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2369
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2370
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2370
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2371
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2371
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacgacaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctatctgg agccattgat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgtga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2372
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2372
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Asp Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2373
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2373
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2374
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2374
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2375
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2375
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctctctgg agccattgat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2376
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2376
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2377
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2377
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcatga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2378
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2378
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2379
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2379
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgccca agctctctgg agccattgat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2380
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2380
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2381
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2381
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt cttcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2382
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2382
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2383
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2383
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagcaggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctatctgg agccagagat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgtga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2384
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2384
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Gln
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2385
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2385
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt cttcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2386
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2386
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2387
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2387
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctatctgg agccagagat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2388
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2388
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2389
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2389
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctatctgg agccattgat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2390
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2390
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Leu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2391
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2391
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctatctgg agccagagat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2392
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2392
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2393

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2393
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcatga tgcagaagaa cgcgcagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2394
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2394
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Ala Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2395
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2395
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctctctgg agccagagat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2396
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2396
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2397
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2397
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcatga tgcagaagaa cgcgcagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2398
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2398
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Ala Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2399
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2399
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggca ttatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctatctgg agccagagat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgcagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2400
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2400
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp His Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Ala Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2401
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2401
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240

ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctatctgg agccagagat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcatga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2402
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2402
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2403
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2403
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2404
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2404
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2405
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2405
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctctctgg agccattgat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2406
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2406
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2407
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2407
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcatga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2408
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2408
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser His Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2409
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2409
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2410
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2410
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2411
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2411
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2412
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2412
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2413
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2413
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagagat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2414
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2414
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2415
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2415
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt cttcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctctctgg agccattgat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2416
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2416
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2417
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2417
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgcttctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2418
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2418
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2419
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2419
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgc attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2420
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2420
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2421
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2421
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga atatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctatctgg agccagagat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgtga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgt ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2422
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2422
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Tyr Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Val Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2423
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2423
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctctctgg agccattgat cgaaagcctg 1620
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gatgtgggca atagtcgtga tgcagaagaa cgcgcagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcataacgta ccgatggag 2379

<210> 2424
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2424
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Leu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Ala Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Asn Val Pro Met Glu
785 790

<210> 2425
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2425
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcactgat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctgccc 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagcg ggtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca cgctctctgg agccagagat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa agactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2426
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2426
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Thr Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Pro Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Arg Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Arg Ser Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 2427
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2427
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca agctatctgg agccagagat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatata cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgcggta ccgatggag 2379

<210> 2428

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2428
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Tyr Leu Glu Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2429
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2429
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc tctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgt attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcggagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggac 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2430
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2430
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Gly Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2431
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2431
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2432
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2432
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2433
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2433
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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cttgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2434
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2434
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Leu Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2435
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2435

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gcatgaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2436
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2436
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro His
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2437
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2437
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacaa ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2438
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2438
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Lys Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2439
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2439
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
aaggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2440
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2440
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2441
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2441
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2442
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2442
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2443
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2443
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatggttag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2444
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2444
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Val Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2445
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2445
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc gggcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2446
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2446
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Gly His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2447
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2447
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacagcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2448
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2448
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2449
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2449
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatatgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2450
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2450
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Met Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2451
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2451
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacac tgactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2452
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2452
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Thr Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2453
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2453
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcg ggggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2454
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2454
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Gly Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2455
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2455
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca cgggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2456
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2456
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Thr Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2457
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2457
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcacatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaatggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2458
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2458
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Thr Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Trp
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2459
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2459
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaagtggg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2460
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2460
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Val Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2461
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2461
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc ggtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2462
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2462
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Arg Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2463
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2463
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gggtgaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2464
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2464
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2465
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2465
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc ggctgaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2466
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2466
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2467
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2467
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttccttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2468
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2468
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Leu Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2469
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2469
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc atggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2470
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2470

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2471
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2471
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaagct gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2472
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2472
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ala Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2473
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2473
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cagcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2474
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2474
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Gln His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2475
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2475
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaaggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2476
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2476
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Arg
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2477
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2477
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2478
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2478
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2479
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2479
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgcg 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2480
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2480
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Ala Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2481
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2481
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacgt ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2482
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2482
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Val Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2483
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2483
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcaccg ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2484
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2484
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2485
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2485
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gcaggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2486
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2486
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2487
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2487
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga ggcgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt tagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2488
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2488
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Ala Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2489
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2489
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aagcgcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2490
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2490
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2491
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2491
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaagtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2492
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2492
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2493
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2493
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatcttcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2494
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2494
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Leu Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2495
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2495
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc tgtcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2496
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2496
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Cys His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2497
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2497
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gtttgaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2498
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2498
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Phe
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2499
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2499
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacat tgactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2500
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2500
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2501
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2501
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggtcc gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgtgatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgccgaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgctgctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatgg ctagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa cgtctggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2502
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2502
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Pro Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Leu Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ala Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Arg Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2503

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2503
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg ccttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagcct 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2504
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2504
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2505
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2505
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gatggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgcaccgt 240
ccgcgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagcct 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcccg tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gataggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2506
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2506
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Met Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala His Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2507
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2507
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gatggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ggtcgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaatat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gataagcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2508
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2508
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Met Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Gly Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Tyr Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Lys Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2509
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2509
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2510
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2510
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2511
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2511
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ccgcgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaatat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2512
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2512
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Tyr Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2513
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2513
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gatggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagcct 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2514
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2514
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Met Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2515
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2515
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg ccttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgttcggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatgggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2516
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2516
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2517
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2517
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgcaccgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgcaaa atagtaggga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatgggcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2518
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2518
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala His Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2519
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2519
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gatggaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg ccttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagcct 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcccg tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggcga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2520
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2520
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Met Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Ala Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2521
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2521
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ggtcgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaatat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatgggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2522
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2522
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Gly Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Tyr Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2523
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2523
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgcaccgt 240
ggtcgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgttcggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatgggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2524
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2524
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala His Arg
65 70 75 80
Gly Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2525
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2525
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ggtcgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgttcggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatgggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2526
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2526
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Gly Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2527
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2527
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagcct 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2528
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2528
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2529
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2529
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg ccttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcag cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2530
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2530
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2531
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2531
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgcaccgt 240
atacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagcct 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gataggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2532
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2532
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala His Arg
65 70 75 80
Ile Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2533
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2533
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgcaccgt 240
ccgcgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg ccttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2534
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2534
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1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala His Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2535
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2535
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgttcggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatgggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2536
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2536
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 2537
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2537
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaatat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatgggcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2538

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2538
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Tyr Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2539
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2539
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctggaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
atacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gataggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2540
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2540
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Ile Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Trp Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2541
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2541
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2542
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2542
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2543
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2543
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cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcgcattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2544
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2544
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala His Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2545
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2545

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2546
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2546
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2547
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2547
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180

tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcatct ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2548
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2548
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2549
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2549
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatccgt cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2550
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2550
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Arg Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2551
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2551
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcgtt cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2552
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2552
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Val Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2553
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2553
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagcggta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2554
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2554
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2555
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2555
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcgtcgtttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2556
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2556
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Ser Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2557
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2557
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatacg 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2558
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2558
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Thr Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2559
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2559
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt ccggttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2560
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2560
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Arg Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2561
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2561
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2562
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2562
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Gly Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2563
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2563
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
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atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2564
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2564
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Glu Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2565
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2565
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcgacttttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2566
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2566
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Thr Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2567
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2567
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatctcg cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2568
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2568
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Ser Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2569
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2569
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttgctaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2570
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2570
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ala Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2571
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2571
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttg ggcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2572
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2572
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Trp Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2573
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2573
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggactgtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2574
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2574
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Thr Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2575
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2575
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggttct ggcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2576
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2576
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Leu Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2577
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2577
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatattc cgggatccgt ggtgggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
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gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2578
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Sucrose Synthase

<400> 2578
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Trp Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2579
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2579
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatccat cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2580
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2580

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile His Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2581
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2581
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gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2582
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2582
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Leu Ser Gln Arg Asp Ser Trp Leu

20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2583
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2583
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
gtgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2584
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2584
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2585
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2585
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatggct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2586
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2586
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Trp Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2587
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2587
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcaat cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2588
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2588
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Asn Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2589
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2589
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaact ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2590
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2590
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2591
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2591
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt ccagttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2592
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2592
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gln Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2593
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2593
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacaga cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagct tccggaaggc tatcccgaag atattggttg gctcgaagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ccacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg ttagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgagcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttcagaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatc 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgccca tcgtctctgg agccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatcaa cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtcgcga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 2594
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Sucrose Synthase

<400> 2594
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
Gln Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Glu Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Ser Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Gln Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Pro Ser Ser Leu Glu Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Gln Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Arg Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 2595
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2595
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aacagatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200

accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2596
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2596
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro

325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2597
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2597
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttagag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2598
<211> 451

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2598
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380

Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Arg Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2599
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2599
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2600
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2600

Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn

435 440 445
Lys Tyr Lys
450

<210> 2601
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2601
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aacagatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2602
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2602
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr

50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2603
<211> 1356

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2603
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caactttctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtaca 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aagtaa 1356

<210> 2604
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2604
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110

Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2605
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2605

atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg aaggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2606
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2606
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys

165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2607
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2607
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420

ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2608
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2608
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220

Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2609
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2609
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840

ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2610
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2610
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val

275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2611
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2611
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtaca 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260

attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2612
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2612
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335

Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2613
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2613
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2614
<211> 451
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2614
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu

385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2615
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2615
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2616
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2616
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val

1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445

Lys Tyr Lys
450

<210> 2617
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2617
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc acgattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2618
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2618
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60

Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2619
<211> 1353
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2619
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgt 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcattg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accattagag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2620
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2620
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln

115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met His Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Arg Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2621
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2621
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60

tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactatctg 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aacagatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2622
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2622
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175

Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2623
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2623
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480

aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactatctg 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2624
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2624
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr

225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2625
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2625
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg aaggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
atgggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgt 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900

gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2626
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2626
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285

Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2627
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2627
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320

atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2628
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2628
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu

340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2629
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2629
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgggtatca tgctgatgtg cacgagccgc acgattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtaca 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aacagatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc aaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2630
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2630
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400

Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2631
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2631
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agagggcaat 600
atgggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
acccttagag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2632
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2632
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15

Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Arg Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys

450

<210> 2633
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2633
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
ggaggtatca tgctgatgtg cacgagccgc acgattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2634
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2634
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu

65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2635
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2635
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgatgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2636
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2636
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125

Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2637
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2637
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120

ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtaca 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagacatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2638
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2638
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu

180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2639
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2639
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540

aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
atgggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aacagatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2640
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2640
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240

Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2641
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2641
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
atgggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgt 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttagata ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960

cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2642
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2642
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Met Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu

290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2643
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2643
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactatctg 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aacagatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgaagat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2644
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2644
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350

Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2645
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2645
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgagcatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagaacccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
ggaggtatca tgctgatgtg cacgagccgc accattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttctgg accattttgc accgcagcag cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2646
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2646
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Ser
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Thr Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Gln Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly

405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2647
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2647
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
aaaaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2648
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2648
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn

20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2649
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2649
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
agtaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2650
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2650
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80

Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Ser Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2651
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2651
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
aaaaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaacatgct 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2652
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2652
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys

130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Lys Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu His Ala Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2653
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2653
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180

ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
agtgggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2654
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2654
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Ser Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190

Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2655
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2655
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
aaagggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggggct 600

atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2656
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2656
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Lys Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Ala Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp

245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2657
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2657
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
agtactccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020

ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2658
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2658
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Ser Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300

Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2659
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2659
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct tcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
agtgggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggggct 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2660
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2660
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Ser Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Ala Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp

355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2661
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2661
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct tcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
aaagggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2662
<211> 451
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2662
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Lys Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415

Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2663
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2663
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
agtgggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2664
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2664
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30

Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Ser Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2665
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2665
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
aaagggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaacataac 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2666
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2666
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn

85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Lys Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu His Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2667
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2667
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tatcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttca tcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
agtgggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaagggaac 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2668
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2668
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Tyr Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe His Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140

Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Ser Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2669
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2669
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240

ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttca gcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
agtaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaacatgct 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2670
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2670
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Gln Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Ser Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu His Ala Met Gln Ile Met Leu Met Cys Thr

195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2671
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2671
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttca tcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aaaactccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaagggaac 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660

accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagcct attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2672
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2672
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe His Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255

Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2673
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2673
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct tcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
agtgggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080

attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2674
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2674
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Ser Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly

305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2675
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2675
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttca gcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
agtgggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaacataac 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2676
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2676
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Gln Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Ser Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu His Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365

Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2677
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2677
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
agtgggccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2678
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2678
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Ser Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu

420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2679
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2679
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tatcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttca tcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aaaactccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaacatgct 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2680
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2680
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Tyr Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser

35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe His Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu His Ala Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2681
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2681
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctaccgatt caacttcctg 480
agtactccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaagggaac 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2682
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2682
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95

His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu
145 150 155 160
Ser Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2683
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2683
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tatcttgcgg agggtcatat taacccgttt ttgaatatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcattat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacca taccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttca tcaagcgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta agattctgac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
agtaatccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc agaaggcaat 600
atgcagatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaattggaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggta ccaaagacga gaacagtacg 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaactggcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcgttgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc ctggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagaa cgatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2684
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2684
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Tyr Leu Ala Glu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
His Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe His Gln
115 120 125
Ala Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu

145 150 155 160
Ser Asn Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Glu Gly Asn Met Gln Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Trp Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Asn Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2685
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2685
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgaaagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300

aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgtggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2686
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2686
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Lys Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205

Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Val Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2687
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2687
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720

aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtt 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaaa gcgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2688
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2688
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser

260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Ser Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2689
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2689
atgcaccatc atcatcatca tggcggtagc ggcgcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140

gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aaa 1353

<210> 2690
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2690
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320

Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2691
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2691
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aaa 1353

<210> 2692

<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2692
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu

370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2693
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2693
atgcaccatc atcatcatca tggcggtagc ggcgcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca caaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2694
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2694
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430

Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2695
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2695
atgcaccatc atcatcatca tggcggtagc ggcgcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccagagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactatcta 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtt 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2696
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2696
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45

Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2697

<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2697
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aac 1353

<210> 2698
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2698
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys

100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Asn
450

<210> 2699
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2699
atgcaccatc atcatcatga aggcggtagc ggctcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgtggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aaa 1353

<210> 2700
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2700
Met His His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160

Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Val Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2701
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2701
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat aaagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360

ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtact 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaaa gcgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aac 1353

<210> 2702
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2702
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser

210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Ser Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Asn
450

<210> 2703
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2703
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgaaagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg attgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtt 780

gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2704
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2704
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Lys Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Ile Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270

Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2705
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2705
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca caaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200

accattaaaa gcgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aac 1353

<210> 2706
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2706
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro

325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Ile Lys Ser Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Asn
450

<210> 2707
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2707
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtt 780
gtctatgtgg cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
acccttaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2708
<211> 451

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2708
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ala Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380

Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2709
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2709
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgaaagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca caaaagacga gaacagtacg 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aaa 1353

<210> 2710
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2710

Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Lys Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn

435 440 445
Lys Tyr Lys
450

<210> 2711
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2711
atgcaccatc atcatcatca tggcggtagc ggcgcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtt 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2712
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2712
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr

50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2713
<211> 1353

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2713
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
acccttaaag gcgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2714
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2714
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110

Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Gly Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2715
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2715

atgcaccatc atcatcatca tggcggtagc ggcgcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aaa 1353

<210> 2716
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2716
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys

165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2717
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2717
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2718
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2718
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2719
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2719
atgcaccatc atcatcatca tggcggtagc ggcgcgaccc tgaaagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgtcgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtact 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840

ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2720
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2720
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Lys Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val

275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2721
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2721
atgcaccatc atcatcatca tggcggtagc ggcgcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactatcta 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtgtt 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgcccaa 1200
accattaaag atgtgatgac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260

attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2722
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2722
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335

Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln
385 390 395 400
Thr Ile Lys Asp Val Met Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2723
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2723
atgcaccatc atcatcatca tggcggtagc ggctcgaccc tgaaagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcaa aaagaagatc 180
ccggagaaat acagtgagag catccatctg gttgagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactatcta 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca aaaaagacga gaacagtgtt 780
gtctatgtgt cgtttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accattaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcggcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2724
<211> 451
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2724
Met His His His His His His Gly Gly Ser Gly Ser Thr Leu Lys Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Leu Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Lys Lys Asp
245 250 255
Glu Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu

385 390 395 400
Thr Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2725
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2725
atgcaccatc atcatcatga aggcggtagc ggcgcgaccc tgagagtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca caaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt gctgccaaaa ggcttcctgg aacgcattgg tgatcgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aac 1353

<210> 2726
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2726
Met His His His His His Glu Gly Gly Ser Gly Ala Thr Leu Arg Val

1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445

Lys Tyr Asn
450

<210> 2727
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2727
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcgtg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgatgga aaaggagccg gatgaagaag atccgttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2728
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2728
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60

Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Val
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Met Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2729
<211> 1353
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2729
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caactttctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atccgttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2730
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2730
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln

115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2731
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2731
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60

tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcagtgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgatgaag atccgttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2732
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2732
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Val Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175

Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Asp
180 185 190
Glu Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2733
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2733
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480

aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattgct 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2734
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2734
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Ala

225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2735
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2735
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgtttact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900

gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2736
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2736
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Phe Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285

Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2737
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2737
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg tcgattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320

atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2738
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2738
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Ser Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu

340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2739
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2739
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cgcgggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2740
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2740
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ala Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400

Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2741
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2741
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattcct 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggt 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2742
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2742
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15

Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Pro
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys

450

<210> 2743
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2743
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccggagact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2744
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2744
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu

65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Glu Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2745
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2745
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgt tccgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2746
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2746
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125

Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Val Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2747
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2747
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120

ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttcttg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2748
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2748
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu

180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Leu Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2749
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2749
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgcaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540

aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgctatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2750
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2750
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Ala Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240

Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2751
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2751
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960

cgcgttgtgg accatatggc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2752
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2752
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu

290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Met Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2753
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2753
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcagttttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2754
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2754
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Val Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350

Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2755
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2755
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgatggtgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2756
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2756
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly

405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2757
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2757
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatggtgga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2758
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2758
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn

20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Val Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2759
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2759
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgcggatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2760
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2760
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80

Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2761
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2761
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagac tccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2762
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2762
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys

130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2763
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2763
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180

ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accgttttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2764
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2764
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190

Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp Arg Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2765
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2765
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600

ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg catattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2766
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2766
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp

245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro His Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2767
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2767
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcaggcg cgtattctga accatccgag cacgggtggc 1020

ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2768
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2768
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300

Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Ala Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2769
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2769
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg acgggtttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2770
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2770
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp Gly Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp

355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2771
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2771
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgtatact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg cgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2772
<211> 451
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2772
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30
Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Tyr Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415

Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2773
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2773
atgcaccatc atcatcatca tggcggtagc ggcgctaccc tgcgcgtact gatgtttccg 60
tggcttgcgc tgggtcatat taacccgttt ttgaacatcg ctaaacaact ggccgatcgt 120
ggtttcctga tctatttatg cagtaccctg attaacctcg aaagcatcat caagaagatc 180
ccggagaaat acagtgagag catccatctg gtggagctgc atctgccaga attaccggaa 240
ctgccaccac attaccatac taccaacggt ttaccaccgc atctgaacgg gaccctgcac 300
aaggcactga agatgagcaa gccgaacttt agcaagatcc tgcaaaacct gaagccggac 360
ctggtcatct acgattttct gcaaccgtgg gcagaacatg tcgtaaacga acagaacatc 420
ccggctgtta aaattctaac cagtggtgcg gcactgttta gctacttttt caacttcctg 480
aagcgaccgg gtgtagaatt tccgtttccg gcgatcaacc tgccgaaggt ggaacaggtg 540
aagatgcgcg agatgtttga aaaggagccg gatgaagaag atcgcttagc acctggcaat 600
ggaggtatca tgctgatgtg cacgagccgc gaaattgagg ctaagtacct ggactattgc 660
accgaactga gcaatgtaaa agttgttccg gttggtccgc catttcagga cccgattact 720
aatgatgcgg acgacaaaga actgattgat tggttaggca ccaaagacga gaacagtacg 780
gtctatgtga gctttggcag cgaatacttc ctgagccgtg aagatatgga agaagtcgcg 840
ttcggcctgg agctgagcaa cgtgaacttt atctgggttg cacgctttcc gaaaggcgag 900
gaacagaatc tggaagacgt tctgccaaaa ggcttcctgg aacgcattgg tgaacgtggt 960
cgcgttgtgg accattttgc accgcagccg tgtattctga accatccgag cacgggtggc 1020
ttcatctctc attgcggttg gaacagcgtc atggaaagca ttgattttgg cgttccgatc 1080
attgcgatgc cgatgcagtg ggatcagccg attaacgcga agctgatcgt ggaattaggc 1140
gttgcagtgg agatcgtgcg tgatgacgat ggcaacattc accgcggcga aattgccgaa 1200
accctgaaag atgtgattac cggcgaaact ggtgagatcc tgcgcggcaa agtacgcgac 1260
attagcaaaa acctgaagag cattcgcgag gaagaaatga atgcagcggc ggaagaactg 1320
atccagctgt gtcgcaacag caacaagtac aag 1353

<210> 2774
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2774
Met His His His His His His Gly Gly Ser Gly Ala Thr Leu Arg Val
1 5 10 15
Leu Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn
20 25 30

Ile Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser
35 40 45
Thr Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr
50 55 60
Ser Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu
65 70 75 80
Leu Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn
85 90 95
Gly Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys
100 105 110
Ile Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln
115 120 125
Pro Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys
130 135 140
Ile Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu
145 150 155 160
Lys Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Pro Lys
165 170 175
Val Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu
180 185 190
Glu Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr
195 200 205
Ser Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser
210 215 220
Asn Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr
225 230 235 240
Asn Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp
245 250 255
Glu Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser
260 265 270
Arg Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val
275 280 285
Asn Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu
290 295 300
Glu Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Glu Arg Gly
305 310 315 320
Arg Val Val Asp His Phe Ala Pro Gln Pro Cys Ile Leu Asn His Pro
325 330 335
Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu
340 345 350
Ser Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp
355 360 365
Gln Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu
370 375 380
Ile Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu
385 390 395 400
Thr Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly
405 410 415
Lys Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu
420 425 430
Met Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn
435 440 445
Lys Tyr Lys
450

<210> 2775
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2775
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gattgccaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcagccccgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2776
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2776
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Ile Ala Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2777
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2777
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg ccatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag acatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2778
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2778
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2779
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2779
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2780
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2780
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2781
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2781
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcataaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg ccatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgagca atgtaaaagt tgttccggtt ggtccgccat atcaggaccc gattaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag acatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2782
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2782
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Tyr Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2783
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2783
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgttcgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc atttcgtgcc gcagccccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2784
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2784
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg

305 310 315 320
Val Val Asp His Phe Val Pro Gln Pro His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2785
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2785
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aggatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaacctc gggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg ccttcgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac aaatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttctggacc atttcgtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2786
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2786
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Phe Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2787
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2787
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgttcgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggtggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2788
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2788
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2789
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2789
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaacctc gggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg ccatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatggccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac aaatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc atttcgcgcc gcaggcccgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2790
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2790
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Ala Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2791
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2791
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgatggaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatggccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac aaatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttctggacc atttcgtgcc gcagcaacgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggtggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2792
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2792
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Ala Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Phe Val Pro Gln Gln Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2793
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2793
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag acatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2794
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2794
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2795
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2795
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgcagg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgttcgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac aaatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc atttcgtgcc gcaggcccgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2796
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2796
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Gln Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Val Pro Gln Ala Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2797
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2797
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aggatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720

gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag acatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atttcgcgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2798
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2798
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2799
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2799
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg ccttcgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat atcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag acatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atttcgtgcc gcagcaacgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2800
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2800
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Tyr Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Phe Val Pro Gln Gln Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2801
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2801
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgttcgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttctggacc atttcgtgcc gcagccccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2802

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2802
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Phe Val Pro Gln Pro His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2803
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2803
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcataaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccgc gggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgttcgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcgggcg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2804
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2804
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ala Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Gly Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2805
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2805
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg ccttcgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggtggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2806
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2806
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2807

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2807
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgttcgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac aaatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atttcgtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2808
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2808
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2809
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2809
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgcagg gtcatattaa cccgtttttg aggatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcataaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccgc gggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg ccatggaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtatcgt ttggcagcga atacttcctg agccgtgaag acatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc atatggcgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgccgaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2810
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2810
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Gln Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ala Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Ala Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2811
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2811
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggtggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2812
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2812
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2813
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2813
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2814
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2814
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2815
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2815
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200

ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2816
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2816
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2817
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2817
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgatagcat ccatctggtt gagctgcatc tgccagaatt gccggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gaccactagc 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2818
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2818
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asp Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Thr Thr Ser
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2819
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2819
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgtgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaagaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2820
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2820

Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asp Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys

435 440 445
Tyr Lys
450

<210> 2821
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2821
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgatagcat ccatctggtt gagctgcatc tgccagaatt gccggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgg aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacgtgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaagaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2822
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2822
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser

50 55 60
Asp Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Glu Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Arg Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2823
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2823
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt gccggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagagcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2824
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2824
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ser Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2825
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2825

atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc cgtattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2826
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2826
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Arg Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2827
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2827
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccagagggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2828
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2828
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Glu Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2829
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2829
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2830
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2830
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2831
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2831
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaagc ttagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2832
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2832
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Leu Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2833
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2833
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agccggaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2834
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2834
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2835
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2835
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcactaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2836
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2836
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Thr Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445

Tyr Lys
450

<210> 2837
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2837
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gcgtatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2838
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2838
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2839
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2839
atgcaccatc atcatgaagg cggtagcggc ggtaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2840
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2840
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2841
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2841
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atgtgtgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2842
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2842
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Val Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2843
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2843
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gggtatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2844
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2844
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2845
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2845
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tactggaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2846
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2846
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2847
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2847
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaagatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320

cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2848
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2848
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Lys Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2849
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2849
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2850
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2850
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2851
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2851
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccacatggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2852
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2852
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro His Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys

450

<210> 2853
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2853
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctt gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2854
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2854
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2855
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2855
atgcaccatc atcatgaagg cggtagcggc cagaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2856
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2856
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2857
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2857
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg taccttttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2858
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2858
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2859
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2859
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtttaag 1350

<210> 2860
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2860
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Phe Lys
450

<210> 2861
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2861
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgtgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960

gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2862
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2862
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2863
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2863
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc gtaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2864
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2864
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2865
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2865
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagaccctaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggaaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2866
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2866
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Pro
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2867
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2867
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggtg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2868
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2868
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Val Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2869
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2869
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcttgatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2870
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2870
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Leu Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2871
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2871
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaaagtgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2872
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2872
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Ser Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2873
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2873
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180

gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc ggggactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2874
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2874
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Gly Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2875
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2875
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcgtgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2876
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2876
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Val Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2877
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2877
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtaggg atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2878
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2878
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Arg Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2879
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2879
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gttctagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2880
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2880
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Ser Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2881
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2881
atgcaccatc atcatgaagg cggtagcggc tcgaccctga aagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttttgcag taccctgatt aacctcgaaa gcatcatcaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc gcttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gattactaat 720
gatgcggacg acaaagaact gattgattgg ttaggcacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcattggtga tcgtggtcgc 960
gttgtggacc attttgcacc gcagccgcgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgccgaaacc 1200
ctgaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2882
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2882
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Phe Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Ile Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Arg Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Ile Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Phe Ala Pro Gln Pro Arg Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Glu Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2883
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2883
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2884
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2884
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2885
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2885
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gtataccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gaatggtgcc gcagcaacat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggaggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2886
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2886
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Tyr Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Gln His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2887
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2887
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg cgaacgaaca gaacatcccg 420
gctgttaaaa ttctaacctc gggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac agatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gaatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2888
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2888
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2889
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2889
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgcagg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gaatggtgcc gcaggcgcat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2890
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2890
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Gln Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2891
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2891
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg cgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gaatggtgcc gcaggcgcat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2892
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2892
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2893
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2893
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg cgaacgaaca gaacatcccg 420
gctgttaaaa ttctaacctc gggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc ggaaaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacg gaatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2894
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2894
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Glu Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2895
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2895
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aatatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gaatggtgcc gcagcaacat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggaggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
attaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2896
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2896
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Gln His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Ile Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2897
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2897
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aatatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg cgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg cgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat atcagactcc gatggccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac agatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gaatggtgcc gcaggcgcat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2898
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2898
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Tyr Gln Thr Pro Met Ala Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2899
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2899
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc acatggtgcc gcaggcgcat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2900
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2900
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2901
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2901
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aatatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcagactcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2902
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2902
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2903
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2903
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aatatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaacctc gggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat atcagactcc ggaaaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacg gaatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggaggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgatgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2904
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2904
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Tyr Gln Thr Pro Glu Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2905
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2905
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacg gaatggtgcc gcaggcgcat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2906
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2906
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2907
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2907
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aatatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg cgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720

gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc acatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2908
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2908
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2909
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2909
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcagactcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2910
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2910
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2911
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2911
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgcagg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atggaggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2912

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2912
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Gln Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Gly Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2913
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2913
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgagg cgatggaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gtatgccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc acatggtgcc gcaggcgcat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2914
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2914
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Ala Met Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Tyr Ala Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2915
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2915
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagccg tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2916
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2916
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2917

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2917
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagcgtat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2918
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2918
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Arg Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2919
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2919
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2920
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2920
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2921
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2921
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgcgg 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2922
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2922
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2923
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2923
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2924
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2924
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2925
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2925
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaagcgtga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2926
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2926
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2927
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2927
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc gggaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2928
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2928
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Arg Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2929
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2929
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaaccggaa caagtacaag 1350

<210> 2930
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2930

Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys

435 440 445
Tyr Lys
450

<210> 2931
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2931
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaagtg 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2932
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2932
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser

50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2933
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2933
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcttgtacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2934
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2934
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2935
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2935

atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaaggcgat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2936
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2936
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ala Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2937
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2937
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggta tggaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2938
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2938
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Met Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2939
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2939
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaagaagga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2940
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2940
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Lys
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2941
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2941
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaagaatga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2942
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2942
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Asn
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2943
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2943
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaagttgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2944
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2944
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Leu
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2945
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2945
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtggc gcaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2946
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2946
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Ala Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445

Tyr Lys
450

<210> 2947
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2947
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttcggga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2948
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2948
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60

Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Arg Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2949
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2949
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg aacatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg taaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgacgatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgcggagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2950
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2950
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Asn Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Asp Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2951
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2951
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaac tgagcaaggg gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2952
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2952
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Leu Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2953
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2953
atgcaccatc atcatgaagg cggtagcggc ggtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgaatgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcagtaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2954
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2954
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Ser Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2955
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2955
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaaa tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccacacggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2956
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2956
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro His Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2957
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2957
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaac tgagcaaggg gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320

cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2958
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2958
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Leu Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2959
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2959
atgcaccatc atcatgaagg cggtagcggc agtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg gaactttagc aagatcctgc ggaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2960
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2960
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2961
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2961
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2962
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2962
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys

450

<210> 2963
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2963
atgcaccatc atcatgaagg cggtagcggc agtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccacacggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2964
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2964
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro His Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2965
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2965
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2966
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2966
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2967
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2967
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2968
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2968
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2969
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2969
atgcaccatc atcatgaagg cggtagcggc agtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaac tgagcaagcc aaactttagc aagatcctgc ggaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2970
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2970
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Leu Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2971
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2971
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca gaagatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccacacggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2972
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2972
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Lys Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro His Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2973
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2973
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgctagaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2974
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2974
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2975
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2975
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atctgtgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaaa tgagcaaggg gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2976
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2976
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2977
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2977
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2978
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2978
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2979
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2979
atgcaccatc atcatgaagg cggtagcggc ggtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgaatgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2980
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2980
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2981
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2981
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atctgtgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaac tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgaatgaaca gaagatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2982
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2982
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Leu Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Lys Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2983
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2983
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180

gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaaa tgagcaagcc aaactttagc aagatcctgc ggaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2984
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2984
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2985
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2985
atgcaccatc atcatgaagg cggtagcggc ggtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaac tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccacacggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2986
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2986
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Leu Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro His Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2987
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2987
atgcaccatc atcatgaagg cggtagcggc ggtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaac tgagcaaggg gaactttagc aagatcctgc ggaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca gaagatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2988
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2988
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Leu Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Lys Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2989
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2989
atgcaccatc atcatgaagg cggtagcggc ggtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atgtgtgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2990
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2990
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Val Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2991
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2991
atgcaccatc atcatgaagg cggtagcggc ggtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaaa tgagcaaggg gaactttagc aagatcctgc ggaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccacacggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2992
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2992
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro His Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2993
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2993
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca gaagatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2994
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2994
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Lys Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2995
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2995
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaaa tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccagaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2996
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2996
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Glu Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2997
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2997
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atctgtgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 2998
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2998
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 2999
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 2999
atgcaccatc atcatgaagg cggtagcggc agtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atctgtgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca gaagatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3000
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3000
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Lys Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3001
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3001
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3002
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3002
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3003
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3003
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaaa tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccagaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3004
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3004
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Glu Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3005
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3005
atgcaccatc atcatgaagg cggtagcggc ggtaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgaaagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc ggaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaacgaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccacacggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3006
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3006
Met His His His His Glu Gly Gly Ser Gly Gly Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro His Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3007
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3007
atgcaccatc atcatgaagg cggtagcggc tcgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgaatgaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg taccgtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3008
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3008
Met His His His His Glu Gly Gly Ser Gly Ser Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Asn Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Pro Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3009
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3009
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaaa tgagcaagcc aaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgagca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggaa gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3010
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3010
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ser Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3011
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3011
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaagatcccg 180
gagaaataca gtgagagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc aaactttagc aagatcctgc ggaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagaatttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc aacattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3012
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3012
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Glu Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Arg Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Asn Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3013
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3013
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacatgtcg tgctagaaca gaacatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccgggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgagctg gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3014
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3014
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Asn Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Arg Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Leu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3015
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3015
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3016
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3016
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3017
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3017
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720

gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3018
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3018
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3019
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3019
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3020
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3020
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3021
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3021
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc acatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagaagcag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3022

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3022
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ser Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3023
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3023
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3024
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3024
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3025
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3025
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3026
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3026
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3027

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3027
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc acatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3028
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3028
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3029
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3029
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3030
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3030
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3031
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3031
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3032
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3032
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3033
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3033
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3034
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3034
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3035
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3035
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3036
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3036
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3037
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3037
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagaagcat acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3038
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3038
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3039
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3039
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacg gtctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagaagcat acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3040
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3040

Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp Gly Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys

435 440 445
Tyr Lys
450

<210> 3041
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3041
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3042
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3042
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3043
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3043
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3044
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3044
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3045
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3045

atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3046
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3046
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3047
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3047
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgat acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3048
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3048
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3049
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3049
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc acctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3050
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3050
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3051
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3051
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3052
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3052
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3053
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3053
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gtctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaaacgcag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3054
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3054
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Arg Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3055
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3055
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3056
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3056
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445

Tyr Lys
450

<210> 3057
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3057
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaaaagcat acgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3058
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3058
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3059
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3059
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagacgcat acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3060
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3060
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Arg Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3061
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3061
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3062
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3062
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3063
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3063
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg ggccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagacgcat acgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3064
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3064
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Gly Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Arg Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3065
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3065
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3066
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3066
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3067
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3067
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320

cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3068
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3068
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3069
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3069
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3070
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3070
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3071
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3071
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc acctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3072
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3072
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys

450

<210> 3073
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3073
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtcga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc acctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3074
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3074
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3075
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3075
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3076
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3076
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3077
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3077
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagaagcag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3078
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3078
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ser Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3079
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3079
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagaagcag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3080
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3080
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ser Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3081
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3081
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3082
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3082
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3083
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3083
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3084
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3084
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3085
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3085
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagacgcat acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3086
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3086
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Arg Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3087
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3087
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3088
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3088
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3089
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3089
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaaagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3090
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3090
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3091
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3091
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gaaaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa cgcctacaag 1350

<210> 3092
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3092
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Ala
435 440 445
Tyr Lys
450

<210> 3093
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3093
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3094
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3094
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3095
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3095
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa cgcctacaag 1350

<210> 3096
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3096
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Ala
435 440 445
Tyr Lys
450

<210> 3097
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3097
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacagctggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gaaaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3098
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3098
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3099
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3099
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagcgggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3100
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3100
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Arg Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3101
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3101
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccgag 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3102
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3102
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3103
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3103
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gattatgacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3104
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3104
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Tyr Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3105
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3105
atgcaccatc atcatgaagg cggttgtggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3106
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3106
Met His His His His Glu Gly Gly Cys Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3107
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3107
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgtg attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3108
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3108
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3109
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3109
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3110
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3110
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3111
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3111
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatacg 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3112
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3112
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Thr Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3113
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3113
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaggctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3114
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3114
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Arg Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3115
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3115
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaggctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3116
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3116
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3117
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3117
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3118
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3118
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3119
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3119
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacgtgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3120
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3120
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Val Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3121
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3121
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gccggaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3122
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3122
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3123
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3123
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acatggaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3124
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3124
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Met Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3125
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3125
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3126
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3126
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3127
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3127
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720

gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt cagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3128
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3128
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Gln Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3129
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3129
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgagggta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3130
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3130
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Gly Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3131
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3131
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cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcaagaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3132

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3132
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Lys Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3133
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3133
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaactgggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3134
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3134
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3135
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3135
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
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ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacggc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3136
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3136
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3137

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3137
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cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgtag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atctcgctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3138
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3138
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Ser Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3139
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3139
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gttcgagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3140
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3140
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Ser Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3141
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3141
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcgcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggt cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3142
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3142
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3143
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3143
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga aaaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3144
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3144
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Lys Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3145
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3145
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaagctc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3146
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3146
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Ala Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3147
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3147
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagccg taagtacaag 1350

<210> 3148
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3148
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Arg Lys
435 440 445
Tyr Lys
450

<210> 3149
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3149
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacctgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3150
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3150

Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys

435 440 445
Tyr Lys
450

<210> 3151
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3151
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgacctgt 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3152
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3152
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Cys
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3153
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3153
atgcaccatc atcatgaagg cggtatgggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3154
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3154
Met His His His His Glu Gly Gly Met Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3155
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3155

atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgtc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3156
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3156
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Arg Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3157
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3157
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcct taagtacaag 1350

<210> 3158
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3158
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Leu Lys
435 440 445
Tyr Lys
450

<210> 3159
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3159
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggccgggt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3160
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3160
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3161
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3161
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tccggcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3162
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3162
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Arg Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3163
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3163
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aagatctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3164
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3164
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asp Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3165
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3165
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccctt 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3166
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3166
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Leu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445

Tyr Lys
450

<210> 3167
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3167
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcctg attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3168
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3168
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Leu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3169
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3169
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3170
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3170
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3171
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3171
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgtt 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3172
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3172
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Val Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3173
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3173
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccccg 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3174
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3174
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Pro

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3175
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3175
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccgtg 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3176
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3176
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Val
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3177
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3177
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagcgtctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320

cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3178
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3178
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Arg Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3179
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3179
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gaaaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc gaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcatctacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaaggtgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaaacc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gccataaagt acgcgacatt 1260
agcaaaaacc tgaagagcat tcgcgaggag gaaatgaatg cagcggcgga agaactgatc 1320
cagctgtgtc gcaacagcaa caagtacaag 1350

<210> 3180
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3180
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Lys Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Ile Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Val
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Thr
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg His Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Lys Ser Ile Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Ser Asn Lys
435 440 445
Tyr Lys
450

<210> 3181
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3181
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3182
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3182
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys

450

<210> 3183
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3183
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3184
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3184
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3185
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3185
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3186
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3186
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3187
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3187
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcagagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3188
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3188
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3189
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3189
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3190
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3190
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3191
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3191
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacg gtctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3192
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3192
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp Gly Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3193
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3193
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3194
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3194
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3195
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3195
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagcgggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3196
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3196
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Arg Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3197
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3197
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3198
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3198
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3199
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3199
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3200
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3200
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3201
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3201
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3202
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3202
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3203
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3203
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3204
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3204
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3205
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3205
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3206
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3206
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3207
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3207
atgcaccatc atcatgaagg cggtagcggc cagagcctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3208
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3208
Met His His His His Glu Gly Gly Ser Gly Gln Ser Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3209
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3209
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3210
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3210
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3211
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3211
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3212
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3212
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3213
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3213
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagcgggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3214
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3214
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Arg Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3215
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3215
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3216
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3216
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3217
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3217
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3218
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3218
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3219
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3219
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3220
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3220
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3221
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3221
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagcgggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3222
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3222
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Arg Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3223
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3223
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagcgggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacg gtctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcagagt acgcgacatc 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3224
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3224
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Arg Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp Gly Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3225
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3225
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3226
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3226
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3227
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3227
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3228
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3228
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3229
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3229
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3230
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3230
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3231
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3231
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3232
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3232
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3233
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3233
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcagagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3234
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3234
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3235
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3235
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3236
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3236
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3237
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3237
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3238
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3238
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3239
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3239
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3240
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3240
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3241
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3241
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacg gtatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3242

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3242
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp Gly Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3243
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3243
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3244
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3244
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3245
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3245
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3246
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3246
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3247

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3247
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3248
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3248
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3249
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3249
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3250
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3250
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3251
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3251
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3252
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3252
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3253
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3253
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacccgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3254
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3254
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3255
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3255
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3256
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3256
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3257
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3257
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3258
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3258
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3259
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3259
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3260
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3260

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys

435 440 445
Tyr Lys
450

<210> 3261
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3261
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagacgcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgccagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3262
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3262
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3263
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3263
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaaggg aaactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgaga 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3264
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3264
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Gly Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Arg Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3265
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3265

atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3266
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3266
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3267
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3267
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3268
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3268
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3269
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3269
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca gggggttccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagcgggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3270
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3270
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Val Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Arg Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3271
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3271
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaacgat tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3272
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3272
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3273
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3273
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaacgac tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3274
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3274
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3275
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3275
atgcaccatc atcatgaagg cggcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3276
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3276
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445

Tyr Lys
450

<210> 3277
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3277
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggattccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3278
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3278
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3279
<211> 1347
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3279
atgcatcatc atgaaggcgg tagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcatctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatga gcaagcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttaaaattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtgtag agtttccgtt tccggcgatc aacctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatggaggt 600
atcatgctga tgtgcacgag ccgcgaaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt ccgccatttc aggacccgat gaccaatgat 720
gcggacgaca aagaactgat tgattggtta ggtaccaaag acgagaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt cgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaggaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
gtggaccata tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgaagctga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggcga aactggtgag atcctgcgcg gcaaagtacg cgacattagc 1260
aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacag 1320
ctgtgtcgca accgcaacaa gtacaag 1347

<210> 3280
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3280
Met His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp

115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn Asp
225 230 235 240
Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys Tyr
435 440 445
Lys

<210> 3281
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3281
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcacaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3282
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3282
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro His Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3283
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3283
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480

actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcccaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3284
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3284
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Pro Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3285
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3285
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcacaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3286
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3286
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro His Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3287
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3287
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3288
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3288
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3289
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3289
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3290
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3290
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3291
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3291
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcccaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3292
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3292
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Pro Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys

450

<210> 3293
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3293
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3294
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3294
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3295
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3295
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcacgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3296
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3296
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro His Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3297
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3297
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3298
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3298
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3299
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3299
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcccaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3300
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3300
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Pro Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3301
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3301
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3302
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3302
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3303
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3303
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3304
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3304
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3305
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3305
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3306
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3306
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3307
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3307
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcccaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3308
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3308
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Pro Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3309
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3309
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcacgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3310
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3310
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro His Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3311
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3311
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3312
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3312
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3313
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3313
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcccaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3314
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3314
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Pro Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3315
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3315
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3316
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3316
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3317
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3317
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
ttcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3318
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3318
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Phe Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3319
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3319
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3320
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3320
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3321
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3321
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagtacc tcccaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3322
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3322
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Val Pro Pro Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3323
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3323
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3324
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3324
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3325
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3325
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3326
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3326
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3327
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3327
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcacgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3328
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3328
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro His Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3329
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3329
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3330
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3330
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3331
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3331
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3332
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3332
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3333
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3333
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcacaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3334
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3334
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro His Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3335
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3335
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3336
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3336
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3337
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3337
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3338
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3338
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3339
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3339
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcccaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3340
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3340
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Pro Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3341
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3341
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3342
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3342
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3343
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3343
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3344
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3344
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3345
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3345
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3346
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3346
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3347
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3347
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720

gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3348
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3348
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3349
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3349
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3350
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3350
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3351
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3351
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3352

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3352
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3353
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3353
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3354
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3354
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3355
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3355
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cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3356
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3356
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3357

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3357
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3358
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3358
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3359
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3359
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3360
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3360
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160

Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3361
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3361
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3362
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3362
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3363
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3363
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3364
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3364
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3365
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3365
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3366
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3366
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3367
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3367
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3368
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3368
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3369
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3369
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3370
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3370

Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys

435 440 445
Tyr Lys
450

<210> 3371
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3371
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3372
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3372
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3373
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3373
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgaag 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3374
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3374
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Lys
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3375
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3375

atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tcacaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3376
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3376
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro His Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3377
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3377
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtat 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3378
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3378
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Tyr Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3379
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3379
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcatca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3380
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3380
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe His Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3381
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3381
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3382
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3382
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3383
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3383
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcttca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
ggcccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagaacatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3384
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3384
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Gly Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Asn Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3385
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3385
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgacgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3386
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3386
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Thr Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445

Tyr Lys
450

<210> 3387
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3387
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcctggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3388
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3388
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Leu Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3389
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3389
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgctggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3390
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3390
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3391
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3391
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgcatgaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3392
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3392
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu His Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3393
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3393
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cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaatttggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3394
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3394
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Phe Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3395
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3395
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcctggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3396
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3396
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Leu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3397
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3397
atgacgcatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3398
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3398
Met Thr His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3399
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3399
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3400
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3400
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3401
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3401
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3402
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3402
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys

450

<210> 3403
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3403
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccacgtggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3404
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3404
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Arg Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3405
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3405
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggacat gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3406
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3406
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Met Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3407
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3407
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccataa caagtacaag 1350

<210> 3408
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3408
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn His Asn Lys
435 440 445
Tyr Lys
450

<210> 3409
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3409
atgaatcatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3410
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3410
Met Asn His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3411
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3411
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggacgt gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3412
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3412
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3413
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3413
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaatgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3414
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3414
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Asn Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3415
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3415
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3416
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3416
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3417
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3417
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggccgggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3418
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3418
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Arg Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3419
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3419
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacattaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3420
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3420
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Ile
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3421
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3421
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtgcctc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3422
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3422
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Pro His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3423
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3423
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3424
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3424
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3425
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3425
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgatttttgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3426
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3426
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Phe Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3427
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3427
atgagtcatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3428
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3428
Met Ser His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3429
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3429
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattcaggg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3430
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3430
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3431
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3431
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgctgaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3432
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3432
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Ala Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3433
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3433
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgctc gtcaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3434
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3434
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Arg Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3435
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3435
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagctcggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3436
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3436
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Ser Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3437
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3437
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aaggggttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3438
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3438
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Gly Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3439
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3439
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggatc gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3440
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3440
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Asp Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3441
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3441
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagactcgaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3442
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3442
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Ser
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3443
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3443
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggtgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3444
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3444
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Val Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3445
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3445
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacactaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3446
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3446
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Thr
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3447
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3447
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgggaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3448
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3448
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3449
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3449
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agccgtaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3450
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3450
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3451
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3451
atgcaccatc atcatgaagg ctctagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3452
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3452
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3453
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3453
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttattaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3454
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3454
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Ile Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3455
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3455
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattggtgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3456
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3456
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3457
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3457
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720

gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccctaa caagtacaag 1350

<210> 3458
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3458
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Pro Asn Lys
435 440 445
Tyr Lys
450

<210> 3459
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3459
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatggcgaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3460
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3460
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3461
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3461
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agctctaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3462

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3462
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Ser Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3463
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3463
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgttgaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3464
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3464
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Val Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3465
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3465
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggactt gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3466
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3466
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3467

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3467
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcgtggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3468
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3468
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Val Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3469
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3469
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgg tgaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3470
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3470
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Val Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3471
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3471
atgcacattc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3472
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3472
Met His Ile His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3473
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3473
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
aagctgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3474
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3474
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Lys Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3475
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3475
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagtatcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3476
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3476
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Tyr His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3477
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3477
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttctcggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3478
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3478
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Ser Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3479
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3479
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3480
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3480

Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys

435 440 445
Tyr Lys
450

<210> 3481
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3481
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagaccttaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3482
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3482
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Leu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3483
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3483
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaaggtggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3484
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3484
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Gly Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3485
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3485

atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agctgtaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3486
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3486
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Cys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3487
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3487
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcacggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3488
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3488
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Thr Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3489
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3489
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga aactctgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3490
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3490
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Thr Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3491
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3491
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcgcgagagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3492
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3492
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3493
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3493
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3494
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3494
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3495
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3495
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3496
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3496
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 3497
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3497
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3498
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3498
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3499
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3499
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccag cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3500
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3500
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Ser Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3501
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3501
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3502
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3502
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3503
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3503
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtg tagagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3504
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3504
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3505
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3505
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcgcgagagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3506
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3506
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3507
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3507
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3508
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3508
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3509
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3509
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgttaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3510
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3510
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3511
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3511
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3512
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3512
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 3513
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3513
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3514
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3514
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3515
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3515
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgttaggt gagatcctgc gcgggagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3516
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3516
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Leu Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3517
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3517
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgagagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3518
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3518
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3519
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3519
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgttaggt gagatcctgc gcgggagagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3520
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3520
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Leu Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3521
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3521
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3522
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3522
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3523
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3523
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3524
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3524
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3525
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3525
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3526
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3526
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3527
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3527
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgttaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3528
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3528
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3529
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3529
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3530
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3530
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3531
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3531
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3532
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3532
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3533
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3533
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3534
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3534
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3535
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3535
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcgggagagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3536
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3536
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3537
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3537
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgttaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3538
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3538
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3539
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3539
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3540
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3540
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3541
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3541
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaactag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3542
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3542
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3543
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3543
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3544
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3544
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3545
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3545
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3546
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3546
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3547
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3547
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3548
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3548
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3549
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3549
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgactggt gagatcctgc gcgggagagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3550
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3550
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3551
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3551
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3552
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3552
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3553
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3553
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3554
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3554
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3555
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3555
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3556
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3556
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3557
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3557
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cccgttaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3558
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3558
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3559
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3559
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3560
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3560
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3561
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3561
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgctgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3562
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3562
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3563
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3563
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcgggagagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3564
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3564
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3565
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3565
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3566
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3566
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3567
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3567
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720

gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3568
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3568
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3569
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3569
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3570
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3570
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3571
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3571
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3572

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3572
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3573
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3573
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3574
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3574
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3575
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3575
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3576
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3576
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3577

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3577
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3578
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3578
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3579
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3579
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaattaggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3580
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3580
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Leu Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3581
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3581
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgggagagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3582
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3582
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3583
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3583
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3584
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3584
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3585
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3585
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgggaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3586
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3586
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3587
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3587
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tagagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3588
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3588
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3589
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3589
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggcg atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatggc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgag 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gccgcaaagt acgcgacatt 1260
agcaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3590
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3590

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Arg Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 3591
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3591
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttaactag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3592
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3592
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Thr Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3593
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3593
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccatgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3594
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3594
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Met Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3595
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3595

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccccgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3596
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3596
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Pro Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3597
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3597
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct cgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3598
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3598
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ser Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3599
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3599
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccta ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3600
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3600
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3601
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3601
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ctctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3602
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3602
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3603
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3603
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3604
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3604
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3605
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3605
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga acttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3606
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3606
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 3607
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3607
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acagactaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3608
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3608
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3609
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3609
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3610
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3610
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3611
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3611
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttagtgag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3612
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3612
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Val Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3613
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3613
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggctaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3614
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3614
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3615
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3615
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag tacccagatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3616
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3616
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Gln Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3617
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3617
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcattatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3618
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3618
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ile Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3619
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3619
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3620
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3620
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3621
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3621
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttg tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3622
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3622
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Leu Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 3623
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3623
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aagatctggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3624
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3624
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Asp Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3625
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3625
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttctttatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3626
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3626
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Phe Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3627
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3627
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gtctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3628
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3628
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3629
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3629
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3630
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3630
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3631
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3631
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cgtctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3632
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3632
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3633
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3633
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgtgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3634
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3634
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3635
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3635
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
ggggtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3636
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3636
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Gly Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3637
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3637
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3638
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3638
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3639
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3639
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga aattgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3640
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3640
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Ile Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3641
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3641
atgcaccatc atcatgaagg cagcagcggc cagaccctga aggtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3642
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3642
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Lys Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3643
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3643
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaattg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgcgtc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3644
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3644
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3645
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3645
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600

ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
attctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3646
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3646
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Ile Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3647
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3647
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccggcgac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3648
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3648
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ala
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3649
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3649
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
cttcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3650
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3650
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Leu Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3651
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3651
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg tggagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggctaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3652
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3652
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Ala Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3653
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3653
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct catgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattactgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3654
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3654
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3655
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3655
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt catgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcagcgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3656
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3656
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Ser Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3657
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3657
atgcatcata atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcatctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatga gcgctcccaa ctttagcaag atcattcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttaaaattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc aatctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttggaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt ccgccatttc aggatgtcat gaccaatgat 720
gcagacgaca aagaactgat tgattggtta gataccaaac ccgagaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt cgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaggaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgaagctga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttcaaggcga aactggtgag atcctgcgcg cgaaagtacg cgacattagc 1260
aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacag 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3658
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3658
Met His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile Ile
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile Leu
130 135 140

Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn Asp
225 230 235 240
Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3659
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3659
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt catgaccaat 720
gatgcagacg acacagaact gattgattgg ttagatacca aacccataaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattcaagg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3660
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3660
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Thr Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Ile
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3661
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3661
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct catgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3662
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3662
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3663
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3663
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta gacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct catgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaatgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3664
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3664
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Arg Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Asn Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3665
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3665
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta gacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggccc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc tatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaatgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3666
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3666
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Arg Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Asn Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3667
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3667
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt catgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattcaagg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3668
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3668
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3669
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3669
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggccc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt catgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3670
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3670
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3671
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3671
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt catgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaatgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3672
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3672
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Asn Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3673
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3673
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3674
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3674
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3675
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3675
atgcatcatc atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctggccctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300

ctgaagatga gcgctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttaaaattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc aatctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttggaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt ccgccatttc aggatgtcat gaccaatgat 720
gcagacgaca aagaactgat tgattggtta gataccaaac ccgagaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt cgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaggaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgaagctga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggcga aactggtgag atcctgcgcg cgaaagtacg cgacattagc 1260
aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacag 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3676
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3676
Met His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205

Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Asn Asp
225 230 235 240
Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3677
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3677
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggccc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct catgaccaat 720

gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattcaagg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3678
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3678
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3679
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3679
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccttaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattcaagg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3680
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3680
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Leu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3681
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3681
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc tatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattcaagg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3682

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3682
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3683
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3683
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaatgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3684
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3684
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Asn Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3685
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3685
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattcaagg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3686
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3686
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3687

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3687
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggccc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaatgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3688
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3688
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Asn Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3689
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3689
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcttagaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgcacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgcgggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcaaaagt acgcgacatt 1260
cagaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3690
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3690
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu His His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Gln Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3691
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3691
atgtcccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccaggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgcgggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcaagagt acgcgacatt 1260
agtagaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3692
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3692
Met Ser His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Gln Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3693
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3693
atgtcccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc agaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagccaggt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcaaaagt acgcgacatt 1260
agtaaaaatc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3694
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3694
Met Ser His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Gln Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3695
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3695
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3696
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3696
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3697
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3697
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3698
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3698
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3699
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3699
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatggccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3700
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3700

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Ala Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 3701
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3701
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3702
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3702
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3703
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3703
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccaac 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3704
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3704
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3705
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3705

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3706
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3706
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3707
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3707
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3708
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3708
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3709
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3709
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagtatcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3710
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3710
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Tyr His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3711
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3711
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aaccctcaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctgcctc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3712
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3712
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Ser
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Pro His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3713
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3713
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aaccctcaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga aactctgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3714
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3714
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Ser
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Thr Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3715
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3715
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggggccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaac 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctgcctc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3716
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3716
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Gly Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Pro His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 3717
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3717
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctgcctc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3718
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3718
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Pro His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3719
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3719
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaac 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3720
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3720
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3721
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3721
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3722
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3722
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3723
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3723
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaac 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3724
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3724
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3725
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3725
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3726
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3726
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3727
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3727
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccaac 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3728
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3728
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Asn
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3729
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3729
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagtatcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga aactctgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3730
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3730
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Tyr Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Thr Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3731
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3731
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatggccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3732
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3732
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Ala Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 3733
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3733
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3734
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3734
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3735
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3735
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3736
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3736
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3737
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3737
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctgcctc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3738
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3738
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Pro His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3739
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3739
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatggccaac 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3740
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3740
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Ala Asn
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3741
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3741
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatgaccaac 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3742
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3742
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3743
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3743
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctgcctc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3744
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3744
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Pro His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3745
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3745
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3746
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3746
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3747
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3747
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagtatcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatggccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3748
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3748
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Tyr His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Ala Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3749
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3749
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatggccaac 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggatc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3750
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3750
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Ala Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3751
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3751
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgcagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctgcctc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3752
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3752
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Ala Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Pro His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3753
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3753
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga aactctgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3754
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3754
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Thr Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3755
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3755
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatgcggacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3756
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3756
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3757
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3757
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttatggatcc gatggccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3758
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3758
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Met Asp Pro Met Ala Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3759
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3759
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccact 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3760
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3760
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Thr Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3761
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3761
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgctgagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3762
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3762
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Leu Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3763
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3763
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcaga tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3764
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3764
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Asp Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3765
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3765
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcaca gggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3766
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3766
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Gln Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3767
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3767
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggttggatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3768
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3768
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Trp Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3769
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3769
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttcata ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3770
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3770
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val His Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3771
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3771
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaatc ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3772
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3772
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Ser Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3773
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3773
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgcgggcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3774
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3774
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Arg Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3775
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3775
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgtatgcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3776
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3776
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Tyr Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3777
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3777
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
tggatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3778
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3778
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Trp Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3779
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3779
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga acagttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3780
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3780
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Gln Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3781
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3781
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta atgccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3782
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3782
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Met Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3783
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3783
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccccg 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3784
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3784
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser

145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Pro Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3785
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3785
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcatg gggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3786
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3786
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Trp Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3787
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3787
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
atggcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720

gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3788
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3788
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Met Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3789
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3789
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgag 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3790
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3790
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Glu Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3791
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3791
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attgtcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3792

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3792
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Cys Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3793
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3793
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcaggg ggcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3794
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3794
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gly Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3795
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3795
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
aggatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3796
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3796
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Arg Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3797

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3797
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccagacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ctggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3798
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3798
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Ser Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3799
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3799
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcgtca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3800
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3800
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ser Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160

Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3801
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3801
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cctgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3802
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3802
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Pro Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3803
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3803
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtggaca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaca ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3804
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3804
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Thr Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Gln Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3805
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3805
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtgcgatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3806
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3806
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ala Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3807
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3807
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgtgaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3808
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3808
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Val Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3809
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3809
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
gcgatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3810
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3810

Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Ala Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys

435 440 445
Tyr Lys
450

<210> 3811
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3811
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgagtgcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3812
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3812
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Ser Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3813
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3813
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcga cgggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3814
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3814
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Thr Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3815
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3815

atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgcccgg 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3816
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3816
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Arg Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3817
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3817
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgccagaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3818
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3818
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Gln Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3819
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3819
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccgt ggcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3820
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3820
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Trp Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3821
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3821
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgggtgcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3822
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3822
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Gly Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3823
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3823
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttaataa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3824
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3824
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Asn Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3825
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3825
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa tttggaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3826
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3826
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Trp Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445

Tyr Lys
450

<210> 3827
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3827
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgctgtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3828
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3828
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Leu Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3829
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3829
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
tctatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3830
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3830
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Ser Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3831
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3831
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atggttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3832
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3832
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Trp Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3833
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3833
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480

actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgacggcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3834
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3834
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Thr Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn

225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3835
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3835
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg atatgcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3836
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3836
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Met Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3837
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3837
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccgt cgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3838
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3838
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Ser Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3839
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3839
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atttttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3840
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3840
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Phe Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3841
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3841
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgacaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3842
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3842
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Asp Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys

450

<210> 3843
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3843
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg atgttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3844
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3844
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Val Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3845
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3845
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgtttgcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3846
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3846
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Phe Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3847
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3847
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcccgaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3848
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3848
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Pro Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3849
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3849
atgcaccatc atcatgaagg cggtagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttcagca agcgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct accgcttcaa cttcctgtct 480
actccgggtg tagagtttcc gtttccggcg atcaacctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcatt gggcgccgga 600
ggtatcatgc tgatgtgcac gagccgcgaa attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggaccc gatgaccaat 720
gatgcggacg acaaagaact gattgattgg ttaggtacca aagacgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttgtggacc atatggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcggcaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa caagtacaag 1350

<210> 3850
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3850
Met His His His His Glu Gly Gly Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Gln Gln Ala
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Arg Phe Asn Phe Leu Ser
145 150 155 160
Thr Pro Gly Val Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Leu Gly Ala Gly Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Glu Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240

Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Gly Thr Lys Asp Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Val Asp His Met Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Gly Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Lys
435 440 445
Tyr Lys
450

<210> 3851
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3851
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttcggaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3852
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3852
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Arg Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3853
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3853
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaac ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3854
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3854
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3855
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3855
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggctatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3856
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3856
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Tyr Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3857
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3857
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacatgtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3858
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3858
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3859
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3859
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgggt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3860
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3860
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Gly Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3861
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3861
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaactgtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3862
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3862
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Thr Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3863
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3863
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttatcgcc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3864
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3864
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ser Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3865
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3865
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3866
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3866
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3867
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3867
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctggt tccgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3868
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3868
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Val Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3869
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3869
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcgctgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3870
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3870
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ala Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3871
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3871
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3872
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3872
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3873
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3873
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgctaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3874
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3874
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Ala Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3875
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3875
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaagc tgagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3876
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3876
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Ala Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3877
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3877
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgtt gccgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3878
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3878
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Leu Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3879
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3879
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3880
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3880
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3881
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3881
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3882
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3882
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3883
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3883
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaacg tgagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3884
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3884
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3885
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3885
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggctctgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3886
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3886
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3887
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3887
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgggaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3888
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3888
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3889
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3889
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgcgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3890
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3890
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Ala
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3891
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3891
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaattct 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3892
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3892
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3893
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3893
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3894
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3894
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Trp Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3895
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3895
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720
gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3896
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3896
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3897
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3897
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atcaatctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccaat 720

gatgcagacg acaaagaact gattgattgg ttagatacca aacccgagaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg cgaaactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3898
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3898
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Asn Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Asn
225 230 235 240
Asp Ala Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3899
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3899
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3900
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3900
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3901
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3901
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccccaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcgggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3902

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3902
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Pro Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Arg Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3903
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3903
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcattatct atttagttag tacctctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3904
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3904
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ile Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3905
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3905
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttccttatct atttatgtag tacccaaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3906
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3906
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Gln Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3907

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3907
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttccttatct atttagttag tacccaaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtca ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3908
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3908
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Val Ser Thr
35 40 45
Gln Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Thr Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3909
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3909
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtca ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3910
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3910
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Thr Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3911
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3911
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3912
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3912
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3913
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3913
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3914
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3914
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3915
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3915
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcattatct atttatgtag tacccaaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3916
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3916
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ile Ile Tyr Leu Cys Ser Thr
35 40 45
Gln Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3917
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3917
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcattatct atttatgtag tacccaaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3918
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3918
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ile Ile Tyr Leu Cys Ser Thr
35 40 45
Gln Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3919
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3919
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag tacctctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3920
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3920

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 3921
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3921
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3922
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3922
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3923
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3923
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3924
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3924
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3925
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3925

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggcc cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3926
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3926
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Pro Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3927
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3927
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtca ccctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3928
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3928
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Thr Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3929
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3929
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3930
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3930
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3931
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3931
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcattatct atttagttag tacctctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3932
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3932
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ile Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3933
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3933
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3934
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3934
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3935
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3935
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3936
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3936
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 3937
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3937
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3938
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3938
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3939
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3939
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcattatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3940
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3940
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ile Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3941
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3941
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag tacctctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3942
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3942
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3943
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3943
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgtag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3944
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3944
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3945
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3945
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac tggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3946
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3946
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3947
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3947
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3948
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3948
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3949
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3949
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag tacctctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
gtgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3950
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3950
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Val Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3951
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3951
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttccttatct atttatgtag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3952
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3952
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 3953
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3953
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3954
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3954
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3955
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3955
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3956
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3956
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3957
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3957
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttccttatct atttatgtag tacctctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtct gcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3958
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3958
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Cys Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3959
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3959
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag taccctaatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tcctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttggaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atgccggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3960
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3960
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Ala Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3961
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3961
atgcatcatc atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatgt cggctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttccgattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt acgccatttc aggatccaat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta gataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt tgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960

ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgagactga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgaaagtacg cgacatttct 1260
aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacgg 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3962
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3962
Met His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp

290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3963
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3963
atgcatcatc atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatga gcgctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttccgattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt ccgccatttc aggatccgat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta gataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt cgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgagactga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgaaagtacg cgacattagc 1260
aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacgg 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3964
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3964
Met His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350

Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3965
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3965
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3966
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3966
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3967
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3967
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3968
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3968
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3969
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3969
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3970
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3970
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3971
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3971
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3972
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3972
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3973
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3973
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3974
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3974
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3975
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3975
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3976
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3976
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3977
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3977
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3978
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3978
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3979
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3979
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3980
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3980
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3981
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3981
atgcatcata atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaag acctggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatgg cggctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttccgattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt ccgccatttc aggatgtgat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta gataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt tgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgagactga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgagagtacg cgacatttct 1260
agaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacag 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3982
<211> 449
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3982
Met His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Asp Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg Val
405 410 415

Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3983
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3983
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3984
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3984
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3985
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3985
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3986
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3986
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3987
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3987
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3988
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3988
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3989
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3989
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3990
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3990
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3991
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3991
atgcatcata atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaag acctggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatgt cggctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttaagattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660

ctgaccaatg taaaagttgt tccggttggt acgccatttc aggatccaat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta gataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaact tgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgagactga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgagagtacg cgacatttct 1260
aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacag 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3992
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3992
Met His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Asp Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255

Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3993
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3993
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 3994
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3994
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 3995
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3995
atgcatcata atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatgg cggctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttccgattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt acgccatttc aggatccaat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta gataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt cgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgagactga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgagagtacg cgacatttct 1260
agaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacag 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3996
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3996
Met His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365

Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg Val
405 410 415
Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3997
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3997
atgcatcata atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatga gcgctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttaaaattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt ccgccatttc aggatccgat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta gataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaact tgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgaagctga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgaaagtacg cgacattagc 1260
aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacag 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 3998
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3998
Met His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn

420 425 430
Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 3999
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 3999
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4000
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4000
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4001
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4001
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4002
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4002
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4003
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4003
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4004
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4004
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4005
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4005
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4006
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4006
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4007
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4007
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aagacctggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc aatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4008
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4008
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Asp Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4009
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4009
atgcatcata atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaag acctggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatga gcgctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttccgattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt acgccatttc aggatttgat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta gataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaagt cgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgaaactga tcgtggaatt aggcgttgca 1140

gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgagagtacg cgacatttct 1260
agaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacgg 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 4010
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4010
Met His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Asp Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Leu Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320

Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335
Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg Val
405 410 415
Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 4011
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4011
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga acttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4012

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4012
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4013
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4013
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4014
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4014
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4015
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4015
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4016
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4016
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4017

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4017
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga acttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4018
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4018
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4019
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4019
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4020
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4020
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4021
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4021
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4022
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4022
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4023
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4023
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aagacctggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4024
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4024
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Asp Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4025
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4025
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga aattgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4026
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4026
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Ile Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4027
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4027
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga acttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4028
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4028
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4029
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4029
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4030
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4030

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 4031
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4031
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4032
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4032
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4033
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4033
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tggcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga aattgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4034
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4034
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Ile Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4035
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4035

atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4036
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4036
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4037
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4037
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420

gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4038
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4038
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4039
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4039
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aagacctggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4040
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4040
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Asp Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4041
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4041
atgcatcatc atgaaggcag cagcggccag accctgagag tactgatgtt tccgtggctt 60
gcgctgggtc atattaaccc gtttttgcgt atcgctaaac aactggccga tcgtggtttc 120
ctgatctatt tatgcagtac cctgattaac ctcgaaagca tcaaaaagag aatcccggag 180
aaatacagta atagcatcca tctggttgag ctgcctctgc cagaattacc ggaactgcca 240
ccacattacc atactaccaa cggtttacca ccgcatctga acgggaccct gcacaaggca 300
ctgaagatgg cggctcccaa ctttagcaag atcctgcaaa acctgaagcc ggacctggtc 360
ctttacgatt ttctgcaacc gtgggcagaa caggtcgtgc tagaacaggg gatcccggct 420
gttccgattc taaccagtgg tgcggcactg tttagctact ttttcaactt cctgaagcga 480
ccgggtcacg agtttccgtt tccggcaatc cgcctgtcga agcgagaaca ggtgaagatg 540
cgcgagatgt ttgaaaagga gccggatgaa gaagatccgt tagcacctgg caatgccggt 600
atcatgctga tgtgcacgag ccgcgtaatt gaggctaagt acctggacta ttgcaccgaa 660
ctgaccaatg taaaagttgt tccggttggt acgccatttc aggatttgat gaccgaagat 720
atcgacgaca aagaactgat tgattggtta ataccaaac ccgaaaacag tgttgtctat 780
gtgtcgtttg gcagcgaata cttcctgagc cgtgaagata tggaagaact tgcgttcggc 840
ctggagctga gcaacgtgaa ctttatctgg gttgcacgct ttccgaaagg cgaagaacag 900
aatctggaag acgttctgcc aaaaggcttc ctggaacgcg ttggtgatcg tggtcgcgtt 960
ctggaccatc tggtgccgca ggcccatatt ctgaaccatc cgagcacggg tggcttcatc 1020
tctcattgcg gttggaacag cgtcatggaa agcattgatt ttggcgttcc gatcattgcg 1080
atgccgatgc agtgggatca gccgattaac gcgagactga tcgtggaatt aggcgttgca 1140
gtggagatcg tgcgtgatga agatggccgg attcaccgcg gcgaaattgc ccaagtcctt 1200
aaagatgtga ttaccggccc cactggtgag atcctgcgcg cgaaagtacg cgacattagc 1260

aaaaacctga gagcgagacg cgaggaggaa atgaatgcag cggcggaaga actgatacgg 1320
ctgtgtcgca accgcaacgc ctacaag 1347

<210> 4042
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4042
Met His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu Met
1 5 10 15
Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile Ala
20 25 30
Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr Leu
35 40 45
Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser Asn
50 55 60
Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu Pro
65 70 75 80
Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly Thr
85 90 95
Leu His Lys Ala Leu Lys Met Ala Ala Pro Asn Phe Ser Lys Ile Leu
100 105 110
Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro Trp
115 120 125
Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile Leu
130 135 140
Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys Arg
145 150 155 160
Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg Glu
165 170 175
Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu Asp
180 185 190
Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser Arg
195 200 205
Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn Val
210 215 220
Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Leu Met Thr Glu Asp
225 230 235 240
Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu Asn
245 250 255
Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg Glu
260 265 270
Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn Phe
275 280 285
Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu Asp
290 295 300
Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg Val
305 310 315 320
Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser Thr
325 330 335

Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser Ile
340 345 350
Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln Pro
355 360 365
Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile Val
370 375 380
Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val Leu
385 390 395 400
Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys Val
405 410 415
Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met Asn
420 425 430
Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala Tyr
435 440 445
Lys

<210> 4043
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4043
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagtcggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga aattgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagagt acgcgacatt 1260
tctagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cggctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4044
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4044
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Ser Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Ile Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Arg Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4045
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4045
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgtcggctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtacgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga acttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
tctaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4046
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4046
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Thr Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 4047
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4047
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agttgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4048
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4048
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Val Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4049
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4049
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagactgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4050
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4050
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Leu Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4051
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4051
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaagctattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4052
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4052
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ala
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4053
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4053
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgtttgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4054
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4054
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Phe Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4055
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4055
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcagga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4056
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4056
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Gln
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4057
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4057
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttagggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4058
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4058
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Arg Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4059
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4059
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa ctggctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4060
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4060
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Trp Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4061
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4061
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcctgt attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4062
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4062
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala Cys Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 4063
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4063
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgtatgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4064
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4064
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Tyr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4065
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4065
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatctatg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4066
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4066
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Tyr Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4067
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4067
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgcctgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4068
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4068
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Pro Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4069
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4069
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtg aggagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4070
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4070
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Glu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4071
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4071
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattcattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4072
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4072
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile His Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4073
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4073
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcaggg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4074
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4074
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Arg Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4075
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4075
atgcacaatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4076
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4076
Met His Asn His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4077
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4077
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgtc gcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4078
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4078
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4079
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4079
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtt ttgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4080
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4080
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Phe Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4081
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4081
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgcct aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4082
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4082
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Pro Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4083
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4083
atgcaccatc atcatgaagg ccggagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4084
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4084
Met His His His His Glu Gly Arg Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4085
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4085
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgggtgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4086
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4086
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Gly Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4087
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4087
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgatggaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4088
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4088
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Met Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4089
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4089
atgcaccatc atcatgaagg cgttagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4090
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4090
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4091
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4091
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattggttgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4092
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4092
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Gly Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4093
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4093
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcggtg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4094
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4094
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Gly Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4095
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4095
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatgc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4096
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4096
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Ala Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4097
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4097
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatccatg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4098
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4098
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile His Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4099
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4099
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcagtg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4100
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4100
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Ser Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4101
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4101
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtt tggagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4102
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4102
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Leu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4103
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4103
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggattt gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4104
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4104
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4105
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4105
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaatttc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4106
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4106
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Phe Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4107
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4107
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcctga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4108
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4108
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Pro
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4109
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4109
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctggtg aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4110
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4110
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr

35 40 45
Leu Val Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4111
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4111
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagacgga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4112
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4112
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Thr
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4113
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4113
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg ctgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4114
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4114
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly Ala Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4115
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4115
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

ctgctgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4116
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4116
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Leu Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4117
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4117
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gactgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4118
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4118
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Thr Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4119
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4119
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactggcga atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4120
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4120
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ala Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4121
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4121
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgctga atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcggcg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4122

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4122
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Leu Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Gly Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4123
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4123
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaacg tgggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4124
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4124
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Arg Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4125
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4125
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgac gcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4126
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4126
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45

Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Thr Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4127

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4127
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
tataaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4128
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4128
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Tyr Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4129
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4129
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgtt 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4130
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4130
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Val
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4131
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4131
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
aataaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4132
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4132
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Asn Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4133
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4133
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccgc agcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4134
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4134
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Gln Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4135
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4135
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
gcgaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4136
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4136
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Ala Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4137
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4137
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gaggcgtaca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4138
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4138
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Ala Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4139
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4139
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
ctaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4140
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4140

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Leu Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 4141
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4141
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctgacgc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4142
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4142
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Thr His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4143
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4143
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgaca ataaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4144
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4144
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asn Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4145
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4145

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatattaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcctgatct atttatgcag taccctgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg tgctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgcaggaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg attttggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
cttaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4146
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4146
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Ile Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Leu Ile Tyr Leu Cys Ser Thr
35 40 45
Leu Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Val Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Gln Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4147
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4147
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4148
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4148
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4149
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4149
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcagcgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4150
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4150
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4151
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4151
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgctac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4152
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4152
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Ala
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4153
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4153
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4154
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4154
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4155
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4155
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgttttcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4156
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4156
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 4157
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4157
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgttttcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4158
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4158
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4159
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4159
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgttttcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcagctcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4160
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4160
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4161
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4161
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4162
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4162
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4163
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4163
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcagctcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4164
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4164
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4165
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4165
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttatcgcc tggcagcgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4166
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4166
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ser Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4167
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4167
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgttttcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4168
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4168
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4169
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4169
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgctac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4170
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4170
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Ala
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4171
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4171
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgctac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcaactcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4172
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4172
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Ala
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 4173
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4173
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4174
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4174
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4175
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4175
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4176
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4176
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4177
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4177
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4178
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4178
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4179
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4179
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgctac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgttttcgt acttttggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttatcgcc tggcaacgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4180
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4180
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Ala
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ser Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4181
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4181
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4182
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4182
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4183
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4183
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcagctcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4184
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4184
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4185
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4185
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4186
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4186
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4187
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4187
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4188
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4188
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4189
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4189
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4190
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4190
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4191
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4191
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgttttcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4192
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4192
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4193
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4193
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggtac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4194
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4194
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4195
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4195
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgctac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4196
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4196
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Ala
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4197
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4197
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4198
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4198
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4199
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4199
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgctac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcagctcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4200
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4200
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Ala
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4201
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4201
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4202
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4202
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4203
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4203
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4204
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4204
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4205
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4205
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttatcgcc tggcagcgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattactgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4206
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4206
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ser Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4207
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4207
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4208
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4208
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4209
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4209
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4210
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4210
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4211
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4211
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgttttcgt acatgttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcgcc tggcagcgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4212
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4212
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4213
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4213
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag tacctcgatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacccgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacatgtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4214
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4214
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ser Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Pro
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu His Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4215
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4215
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcgc gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggt cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4216
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4216
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4217
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4217
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttgaaaa agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4218
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4218
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4219
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4219
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttgcaaa agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4220
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4220
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Ala Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4221
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4221
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4222
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4222
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4223
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4223
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttgaaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4224
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4224
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Glu Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4225
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4225
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttgcaaa agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4226
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4226
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Ala Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4227
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4227
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttgcaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4228
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4228
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Ala Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4229
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4229
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
ctgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4230
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4230
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Leu Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4231
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4231
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttgcaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4232

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4232
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Ala Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4233
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4233
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggttaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4234
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4234
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4235
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4235
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
atgcgcgaga tgtttgcaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4236
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4236
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Met Arg Glu Met Phe Ala Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4237

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4237
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggttaag 540
ctgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4238
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4238
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Leu Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4239
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4239
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttggaaa agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4240
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4240
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4241
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4241
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
atgcgcgaga tgtttgcaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4242
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4242
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Met Arg Glu Met Phe Ala Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4243
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4243
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4244
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4244
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4245
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4245
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4246
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4246
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4247
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4247
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttgaaaa agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4248
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4248
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4249
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4249
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4250
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4250

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 4251
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4251
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggttaag 540
ctgcgcgaga tgtttgcaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4252
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4252
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Leu Arg Glu Met Phe Ala Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4253
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4253
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagactaag 540
ctgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4254
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4254
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Thr Lys Leu Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4255
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4255

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4256
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4256
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4257
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4257
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420

gctgttaaag ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4258
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4258
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4259
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4259
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccga ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4260
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4260
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4261
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4261
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
ctgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4262
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4262
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Leu Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4263
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4263
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggttaag 540
ctgcgcgaga tgtttgcaaa agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4264
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4264
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Leu Arg Glu Met Phe Ala Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4265
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4265
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaaac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4266
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4266
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 4267
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4267
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
ctgcgcgaga tgtttgcaaa agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcagaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4268
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4268
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Leu Arg Glu Met Phe Ala Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Arg Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4269
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4269
atgcaccatc ataatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcattc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggttaag 540
atgcgcgaga tgtttggaag agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4270
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4270
Met His His His Asn Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ile Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Gly Arg Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4271
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4271
atgcaccatc atcatgaagg cagcagcggc cagttgctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4272
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4272
Met His His His His Glu Gly Ser Ser Gly Gln Leu Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4273
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4273
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaatttacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4274
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4274
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Phe Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4275
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4275
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcggt 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4276
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4276
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gly Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4277
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4277
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gattaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4278
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4278
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4279
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4279
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa tccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4280
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4280
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Asn Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4281
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4281
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tagtgatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4282
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4282
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Ser Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 4283
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4283
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaca tagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4284
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4284
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys His Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4285
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4285
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4286
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4286
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4287
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4287
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatctgat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc atgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4288
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4288
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Leu Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4289
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4289
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccttaag 1350

<210> 4290
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4290
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 4291
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4291
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgagtc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4292
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4292
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ser Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4293
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4293
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgccta tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc ggtgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4294
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4294
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Met Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Val Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4295
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4295
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagcttcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4296
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4296
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Leu Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4297
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4297
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccaaggt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4298
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4298
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro Arg Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4299
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4299
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtcggagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4300
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4300
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Arg Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4301
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4301
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg cactactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4302
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4302
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Thr Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4303
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4303
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgctgatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4304
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4304
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Ala Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4305
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4305
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta cgtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4306
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4306
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Thr Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4307
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4307
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gggtaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4308
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4308
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Gly Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4309
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4309
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaggggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4310
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4310
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gly Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4311
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4311
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaagtcatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4312
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4312
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Ser His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4313
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4313
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtcc tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4314
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4314
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Pro Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4315
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4315
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccataag 1350

<210> 4316
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4316
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
His Lys
450

<210> 4317
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4317
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc ggcgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4318
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4318
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ala Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4319
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4319
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacgtt 1350

<210> 4320
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4320
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Val
450

<210> 4321
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4321
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaactggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4322
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4322
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Thr Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4323
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4323
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaagg gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4324
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4324
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Gly Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4325
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4325
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagggggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4326
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4326
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Gly Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4327
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4327
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgcaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4328
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4328
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Gln Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4329
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4329
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc gcgattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4330
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4330
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Ala Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4331
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4331
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatcc atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4332
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4332
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4333
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4333
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgcag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4334
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4334
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Gln

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4335
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4335
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4336
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4336
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4337
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4337
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cttattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4338
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4338
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Leu Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4339
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4339
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4340
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4340
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4341
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4341
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca gaagatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4342

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4342
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Lys Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4343
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4343
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgctct 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4344
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4344
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Ser Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4345
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4345
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcagactcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4346
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4346
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Thr Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4347

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4347
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gagtaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4348
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4348
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ser Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4349
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4349
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct cgttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaac ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4350
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4350
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Ser Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4351
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4351
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtcagagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4352
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4352
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gln Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4353
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4353
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcggggt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4354
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4354
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Gly Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4355
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4355
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc gttattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4356
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4356
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Val Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4357
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4357
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acatgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4358
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4358
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val His Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4359
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4359
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt actggactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4360
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4360

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr Trp Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 4361
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4361
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccgaggaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4362
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4362
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Glu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4363
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4363
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca gacgatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4364
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4364
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Thr Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4365
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4365

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcggt 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4366
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4366
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Gly Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4367
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4367
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4368
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4368
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4369
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4369
atgcaccatc atcatgaagg cagcagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4370
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4370
Met His His His His Glu Gly Ser Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4371
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4371
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt agcggacatt 1260

agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4372
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4372
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Ala Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4373
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4373
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggctc attacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4374
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4374
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala His Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4375
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4375
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactggata atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4376
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4376
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Asp Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 4377
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4377
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctgtgg gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4378
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4378
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Trp Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4379
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4379
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gcggaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4380
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4380
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Arg Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4381
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4381
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcctc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4382
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4382
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile Pro Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4383
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4383
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtggtagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4384
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4384
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4385
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4385
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gttgtagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4386
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4386
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Cys Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4387
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4387
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcgggaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4388
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4388
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Gly Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4389
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4389
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgtggaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4390
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4390
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Val Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4391
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4391
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggtgcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4392
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4392
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Val Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 4393
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4393
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgcata tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4394
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4394
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu His Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4395
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4395
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgattgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactaata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4396
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4396
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Ile Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4397
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4397
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccttactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4398
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4398
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Leu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4399
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4399
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaacc gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540

atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4400
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4400
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Pro Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4401
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4401
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagtgggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4402
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4402
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Val Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4403
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4403
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctga ttaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4404
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4404
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Ile Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4405
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4405
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc tttatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4406
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4406
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Phe Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4407
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4407
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgccagtaag 1350

<210> 4408
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4408
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Ser Lys
450

<210> 4409
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4409
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccacgtggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4410
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4410
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Arg Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4411
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4411
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgctggaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4412
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4412
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Leu Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4413
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4413
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcttgaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4414
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4414
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Leu Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4415
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4415
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgact 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4416
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4416
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Thr
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4417
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4417
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgag tccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4418
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4418
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Ser Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4419
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4419
atgcaccatc atcatgaagg cagcagcggc cagattctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4420
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4420
Met His His His His Glu Gly Ser Ser Gly Gln Ile Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4421
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4421
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattactc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4422
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4422
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile Thr Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4423
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4423
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt aatggacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4424
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4424
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Met Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4425
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4425
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccgtaag 1350

<210> 4426
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4426
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Arg Lys
450

<210> 4427
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4427
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agccttaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4428
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4428
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Leu Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4429
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4429
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtacaggt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4430
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4430
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Gln Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4431
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4431
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgagccg gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4432
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4432
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Pro Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4433
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4433
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcgctaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4434
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4434
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ala Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4435
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4435
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatccgtaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4436
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4436
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Arg Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4437
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4437
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaat 1350

<210> 4438
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4438
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Asn
450

<210> 4439
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4439
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtcctagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4440
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4440
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Pro Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4441
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4441
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcagtc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4442
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4442
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Ser Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4443
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4443
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgattgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4444
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4444
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Leu Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4445
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4445
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctggat 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4446
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4446
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Asp
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4447
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4447
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtcg ggaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4448
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4448
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Arg Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4449
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4449
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aaccccggaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4450
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4450
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Arg
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4451
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4451
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4452

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4452
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4453
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4453
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttct gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4454
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4454
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Leu Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4455
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4455
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatctgt 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4456
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4456
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Cys Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4457

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4457
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagggtctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4458
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4458
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Gly Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4459
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4459
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcaataag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4460
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4460
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Asn Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4461
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4461
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagcgtctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4462
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4462
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Arg Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4463
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4463
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc agtattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4464
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4464
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Ser Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4465
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4465
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgg ggaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4466
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4466
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gly Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4467
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4467
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gacgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4468
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4468
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Thr Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4469
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4469
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gaggtgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4470
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4470

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Val Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 4471
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4471
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca gtcgatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4472
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4472
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Ser Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4473
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4473
atgcaccatc atcatgaagg cagcagcggc gataccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4474
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4474
Met His His His His Glu Gly Ser Ser Gly Asp Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4475
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4475

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgtatgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4476
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4476
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Val Lys Met Tyr Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4477
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4477
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420

gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagctggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4478
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4478
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Ala Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4479
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4479
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccatctggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4480
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4480
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Ser Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4481
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4481
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaaaacc tgagagcgag acgcgatgag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4482
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4482
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Asp Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4483
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4483
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcaggaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4484
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4484
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Gln Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4485
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4485
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtca ggaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4486
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4486
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Gln Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 4487
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4487
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaccgggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4488
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4488
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4489
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4489
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaattgggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4490
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4490
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Leu Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4491
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4491
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atggtggaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4492
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4492
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Val Lys Met Val Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4493
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4493
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgcgcgaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgccggtaag 1350

<210> 4494
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4494
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Arg Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Gly Lys
450

<210> 4495
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4495
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcctc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctgc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaaa ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggtgaag 540
atgacggaga tgtttgaaaa ggagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgaagc tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaaaacc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcatacaag 1350

<210> 4496
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4496
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Pro Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Ile
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Val Lys Met Thr Glu Met Phe Glu Lys Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Lys Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Asn Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4497
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4497
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccag ccgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4498
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4498
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4499
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4499
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtttaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccac ccgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4500
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4500
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Thr Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4501
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4501
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acttctttaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaatcgattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4502
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4502
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 4503
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4503
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgttttcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4504
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4504
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4505
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4505
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gaggcctaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcgtgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaatcgattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4506
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4506
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Ala Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Val Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4507
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4507
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acttctggaa cttcgtgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4508
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4508
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Trp Asn Phe Val Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4509
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4509
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtttaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gacgtttgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4510
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4510
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Thr Phe Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4511
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4511
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acttctggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcggga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcagcgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gatgacggaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccac gcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4512
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4512
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Thr Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4513
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4513
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acttctttaa cttcgtgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcggga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatct gggaacggaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaagcgattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4514
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4514
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Val Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Leu Gly Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ala
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4515
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4515
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgttttcgt acttctggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcagcgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccac gcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4516
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4516
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Thr Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4517
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4517
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgttttcgt acttctggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcagcgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4518
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4518
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4519
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4519
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acttctggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccac ccgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4520
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4520
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Thr Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4521
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4521
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgttttcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcagga acaggataag 540
ctgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcagcgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4522
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4522
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Gln
165 170 175
Glu Gln Asp Lys Leu Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4523
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4523
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgttttcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcagga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gacgacggaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccag ccgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4524
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4524
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Gln
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Thr Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4525
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4525
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gaggcctaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtttaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcggga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcagcgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaatcgattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4526
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4526
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Ala Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4527
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4527
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcagga acaggataag 540
ctgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccag ccgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4528
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4528
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Gln
165 170 175
Glu Gln Asp Lys Leu Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4529
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4529
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtttaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gacgtttgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4530
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4530
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Thr Phe Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4531
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4531
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgttttcgt acatgtttaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcggga acaggataag 540
ctgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcagcgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gggaacggaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaatcgattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4532
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4532
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Met Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Leu Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Gly Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4533
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4533
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcgtgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcagcgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gggaacggaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattcaggg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4534
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4534
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Val Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Gly Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gln Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4535
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4535
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gaggcctaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcgtgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagccac gcgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4536
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4536
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Ala Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Val Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Thr Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4537
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4537
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaagtaca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttgcgt acatgtggaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4538
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4538
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ala Tyr Met Trp Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4539
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4539
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg aggagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatggacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4540
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4540
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Glu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asp Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4541
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4541
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4542
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4542
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4543
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4543
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctgtc aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaacg ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagggcgat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4544
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4544
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Val Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Arg Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Gly Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4545
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4545
atgcaccacc atcatgaagg ctcgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactggcca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4546
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4546
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Ala Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4547
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4547
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaacg ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg aggagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4548
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4548
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Arg Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Glu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4549
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4549
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4550
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4550
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4551
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4551
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgccaagaag 1350

<210> 4552
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4552
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Lys Lys
450

<210> 4553
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4553
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagctcgcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4554
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4554
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ser Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4555
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4555
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gccgtcgcaa cgcctacaag 1350

<210> 4556
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4556
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4557
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4557
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaactggatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4558
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4558
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Leu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4559
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4559
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgtgg 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4560
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4560
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Trp Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4561
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4561
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttggg aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4562

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4562
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Gly Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4563
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4563
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4564
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4564
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4565
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4565
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aagcgctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4566
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4566
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Ala Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4567

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4567
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaagcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4568
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4568
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Lys Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4569
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4569
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacgggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4570
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4570
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Arg Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4571
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4571
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgagggt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4572
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4572
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4573
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4573
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccagaag 1350

<210> 4574
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4574
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Gln Lys
450

<210> 4575
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4575
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tctcgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4576
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4576
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4577
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4577
atgcaccatc atcatgaagg cagcggtggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4578
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4578
Met His His His His Glu Gly Ser Gly Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4579
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4579
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcaggcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4580
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4580

Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Arg Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 4581
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4581
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcagt 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4582
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4582
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Ser Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4583
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4583
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcgtaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4584
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4584
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu Arg Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4585
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4585

atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccag 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4586
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4586
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4587
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4587
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgcaa cgcctacaag 1350

<210> 4588
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4588
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4589
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4589
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccgctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4590
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4590
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4591
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4591
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gccaggaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4592
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4592
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gln Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4593
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4593
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gttttagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4594
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4594
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Phe Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4595
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4595
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcccgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4596
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4596
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Pro Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 4597
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4597
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagctgatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4598
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4598
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Ala
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4599
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4599
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaattcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4600
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4600
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4601
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4601
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca tgtcaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4602
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4602
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Cys Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4603
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4603
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4604
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4604
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4605
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4605
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgctt ggcctacaag 1350

<210> 4606
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4606
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Leu Ala
435 440 445
Tyr Lys
450

<210> 4607
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4607
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctaaggca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4608
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4608
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Arg Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4609
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4609
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccggaag 1350

<210> 4610
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4610
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Arg Lys
450

<210> 4611
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4611
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagagtctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4612
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4612
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Ser Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 4613
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4613
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca agtcaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4614
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4614
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Ser Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4615
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4615
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaactctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4616
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4616
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Thr Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4617
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4617
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atcggagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4618
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4618
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Arg Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4619
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4619
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctagcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccggat gaaccggatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4620
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4620
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Pro
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4621
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4621
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aaccagaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgccaaggtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4622
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4622
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4623
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4623
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gttgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4624
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4624
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4625
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4625
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acccggaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4626
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4626
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4627
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4627
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4628
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4628
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4629
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4629
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaacggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4630
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4630
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Thr Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4631
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4631
atgcaccatc atcatgaagg cagcagcggc cagtctctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4632
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4632
Met His His His His Glu Gly Ser Ser Gly Gln Ser Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4633
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4633
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagcggctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4634
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4634
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Arg Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4635
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4635
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctga ttgacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4636
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4636
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Ile
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4637
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4637
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccatgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagtaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4638
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4638
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser His
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4639
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4639
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gattaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4640
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4640
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Ile Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4641
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4641
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggag atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4642
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4642
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4643
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4643
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc ataagagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4644
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4644
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Lys Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4645
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4645
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcatg 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4646
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4646
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Met Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4647
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4647
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat cattctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4648
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4648
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile Ile Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4649
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4649
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctatctca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4650
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4650
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Ser Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4651
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4651
atgcaccatc atcatgaagg cagcagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4652
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4652
Met His His His His Glu Gly Ser Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4653
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4653
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc aatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaca tagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4654
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4654
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
His Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4655
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4655
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga attggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4656
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4656
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Leu Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4657
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4657
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4658
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4658
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4659
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4659
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgcgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4660
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4660
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ala Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4661
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4661
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgccttgaag 1350

<210> 4662
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4662
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 4663
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4663
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tctgtcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4664
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4664
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Cys Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4665
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4665
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagggca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4666
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4666
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Gly Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4667
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4667
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatttggacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4668
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4668
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Leu Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4669
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4669
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg cgagactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4670
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4670
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Glu Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4671
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4671
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagatca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4672

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4672
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Asp Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4673
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4673
atgcaccatc atcatgaaca tagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4674
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4674
Met His His His His Glu His Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4675
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4675
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gccatcgcaa cgcctacaag 1350

<210> 4676
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4676
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg His Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4677

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4677
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgcgtgatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4678
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4678
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Arg Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4679
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4679
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4680
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4680
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4681
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4681
atgcaccatc atcatgaagg cagcagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaaggggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgatcgtgga attaggcgtt 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaatg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 4682
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,2-glycosyltransferase"

<400> 4682
Met His His His His Glu Gly Ser Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gly Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Ile Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 4683
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4683
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780

ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4684
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4684
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4685
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4685
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaagttaa agatcttaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagaagat tgctcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggag accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa acacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4686
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4686
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Leu Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Lys Ile Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4687
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4687
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgagagttaa agatattaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat tgctcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctgtcg accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgaacagca gcaacctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggaa ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaat cgtttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4688
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4688
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Arg Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Ser Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Asn Ser Ser Asn Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Glu Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4689
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4689
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaat cgtttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtctga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4690
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4690

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4691
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4691
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaagttaa agatattaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat tgctcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggag accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagtttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4692
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4692
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Ala
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4693
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4693
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaagttaa agatattaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggag accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaac cgtttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagtcgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcatttgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4694
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4694
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Pro
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4695
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4695

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacaatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttcca atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4696
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4696
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Asn Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4697
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4697
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ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4698
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4698
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4699
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4699
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg agggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4700
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4700
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Arg Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4701
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4701
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacagtagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4702
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4702
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Ser Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4703
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4703
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgttgc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4704
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4704
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4705
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4705
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4706
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4706
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4707
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4707
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaat 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4708
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4708
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Asn Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4709
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4709
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4710
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4710
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4711
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4711
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtttgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4712
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4712
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Phe Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4713
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4713
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttgatcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4714
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4714
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Asp Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4715
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4715
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4716
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4716
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4717
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4717
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa ctttccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4718
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4718
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Phe Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4719
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4719
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa ccggccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4720
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4720
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Arg Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4721
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4721
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacattagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4722
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4722
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 4723
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4723
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gaagatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4724
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4724
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Lys Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4725
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4725
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa ccagccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4726
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4726
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Gln Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4727
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4727
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cattccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4728
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4728
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Ile Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4729
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4729
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4730
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4730
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4731
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4731
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgcagtgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4732
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4732
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Gln
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4733
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4733
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cggggccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4734
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4734
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Gly Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4735
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4735
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cgggccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4736
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4736
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Gly Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4737
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4737
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acgttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4738
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4738
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Val Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4739
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4739
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa caagccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4740
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4740
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Lys Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4741
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4741
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa catgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4742
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4742
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Met Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4743
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4743
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta cggatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4744
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4744
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Thr Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4745
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4745
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600

gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacactagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4746
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4746
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Thr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4747
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4747
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cccgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4748
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4748
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Pro Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4749
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4749
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgtct 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4750
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4750
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4751
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4751
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4752
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4752
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4753
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4753
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtatgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4754
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4754
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Tyr Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4755
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4755
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggactatgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4756
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4756
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Tyr Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4757
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4757
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggactctgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4758
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4758
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4759
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4759
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgctg 240

catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4760
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4760
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Leu
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4761
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4761
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtggctga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4762
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4762
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4763
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4763
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttccttggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4764
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4764
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Leu Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4765
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4765
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4766
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4766
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4767
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4767
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acctgaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4768
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4768
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4769
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4769
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcaccatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4770
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4770
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His His Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4771
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4771
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgtgtc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4772
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4772
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Cys Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4773
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4773
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggtttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4774
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4774
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4775
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4775
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggacggtgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4776
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4776
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4777
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4777
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgattc cgctgccgaa gcaccctagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4778
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4778
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Pro Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4779
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4779
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgtatc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4780
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4780
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Tyr Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4781
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4781
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa ccctccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4782

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4782
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Pro Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4783
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4783
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accacggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4784
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4784
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Thr Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4785
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4785
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg ggtgatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4786
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4786
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Val Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4787

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4787
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cgagccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4788
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4788
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Glu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4789
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4789
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
tgtggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4790
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4790
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Cys Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4791
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4791
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cgggccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4792
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4792
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Gly Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4793
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4793
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctggttc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780

ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4794
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4794
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Val Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4795
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4795
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcggg tccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgc ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4796
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4796
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Gly Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4797
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4797
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctggtgc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4798
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4798
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Val Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4799
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4799
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gattatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4800
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4800

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4801
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4801
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gggtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4802
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4802
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4803
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4803
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcactcaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4804
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4804
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4805
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4805

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga ctgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4806
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4806
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4807
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4807
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgtccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4808
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4808
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4809
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4809
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gggtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4810
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4810
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4811
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4811
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc tatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggtgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa cctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgca gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcgaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgaccgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
tgggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4812
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4812
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Gln Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Trp Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4813
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4813
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga ccgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4814
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4814
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4815
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4815
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtttgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4816
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4816
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Phe Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4817
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4817
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gcgccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtgtccga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4818
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4818
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4819
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4819
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4820
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4820
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4821
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4821
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtttgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4822
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4822
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Phe Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4823
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4823
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga ccgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtttgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4824
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4824
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Phe Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4825
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4825
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gcgccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4826
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4826
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4827
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4827
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtttgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4828
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4828
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Phe Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4829
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4829
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4830
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4830
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4831
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4831
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4832
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4832
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 4833
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4833
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4834
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4834
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4835
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4835
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtttgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4836
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4836
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Phe Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4837
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4837
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4838
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4838
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4839
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4839
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4840
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4840
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4841
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4841
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4842
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4842
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4843
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4843
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accctggaga gcgtgtccga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4844
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4844
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4845
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4845
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accatggagg gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4846
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4846
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4847
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4847
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga ccgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4848
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4848
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4849
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4849
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accatggagg gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4850
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4850
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4851
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4851
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accatggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4852
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4852
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4853
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4853
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagccacta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4854
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4854
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4855
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4855
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600

gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga ccgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtgtccga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4856
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4856
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4857
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4857
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggaga gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4858
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4858
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4859
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4859
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtttgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accctggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4860
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4860
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Phe Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Ser Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4861
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4861
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accatggaga gcgtgtccga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4862
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4862
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4863
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4863
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4864
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4864
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4865
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4865
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga ccgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4866
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4866
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4867
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4867
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accatggaga gcgtgtccga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4868
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4868
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4869
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4869
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcacctgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4870
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4870
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Leu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4871
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4871
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgcgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctaca cccacggcgg ttggaacggc 1080
accatggaga gcgtgtccga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4872
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4872
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4873
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4873
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gcgccgaaaa ccagcaacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcagccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga ttcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggaga gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4874
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4874
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ser Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4875
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4875
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4876
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4876
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4877
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4877
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcttca 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctaccgaa gcacataagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgtgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgtcctcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttttgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4878
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4878
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4879
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4879
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctaccgaa gcacgaaagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgtcctcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtgtcaga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4880
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4880
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4881
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4881
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgcttca 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctaccgaa gcactacagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttttgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4882
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4882
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4883
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4883
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctaccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4884
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4884
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4885
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4885
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccatgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttttata cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4886
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4886
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4887
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4887
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aaaccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgatgc cgctaccgaa gcactacagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgtgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttttgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4888
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4888
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4889
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4889
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttttata cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4890
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4890
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Tyr Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4891
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4891
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgtgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4892

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4892
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4893
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4893
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acgttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgtgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtgtcaga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4894
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4894
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Val Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4895
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4895
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccatta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg cgggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctaccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga ccgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttttgga cccacggcgg ttggaacggc 1080
accatggagg gcgtgtcaga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4896
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4896
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Arg Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4897

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4897
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acgttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aaaccgaaaa ccagccatta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctaccgaa gcacataagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4898
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4898
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Val Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4899
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4899
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acgttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctaccgaa gcactacagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accttggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4900
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4900
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Val Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4901
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4901
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4902
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4902
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4903
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4903
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780

ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgggg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgaaagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4904
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4904
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4905
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4905
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtatag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcggatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc aggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaatgcgatt cgtcgtgtga tggttgaccg tgaaggtgaa 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4906
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4906
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Gln Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4907
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4907
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcaggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggctttg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4908
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4908
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4909
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4909
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggctctg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4910
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4910

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Ser Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4911
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4911
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgattcg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacgaggat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggctctg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgattttgg tctcgatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4912
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4912
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Ser Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Ser Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4913
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4913
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggctctg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gagcctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4914
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4914
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Ser Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Ser Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4915
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4915

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtcagatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4916
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4916
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Gln Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4917
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4917
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaatttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4918
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4918
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4919
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4919
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcggtcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4920
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4920
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ser Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4921
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4921
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat tgtgcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4922
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4922
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Val
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4923
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4923
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat tattcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4924
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4924
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Ile
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4925
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4925
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtggagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4926
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4926
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Glu
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4927
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4927
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat tacgcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4928
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4928
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Thr
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4929
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4929
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcgcga gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4930
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4930
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ala Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4931
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4931
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gaggttctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4932
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4932
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Val Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4933
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4933
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaacatgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4934
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4934
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
His Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4935
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4935
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccggatagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4936
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4936
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Asp
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4937
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4937
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacagtgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4938
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4938
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Ser Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4939
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4939
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttccggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4940
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4940
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Pro Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4941
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4941
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc atgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga agatgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4942
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4942
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp His Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asp Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 4943
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4943
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggg ctgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4944
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4944
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Ala Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4945
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4945
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat tgggcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4946
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4946
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Gly
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4947
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4947
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taaggctacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4948
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4948
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Ala Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4949
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4949
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacacggat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4950
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4950
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4951
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4951
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gtgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacctctc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4952
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4952
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Cys Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Ser Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4953
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4953
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat gatacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4954
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4954
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Asp Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4955
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4955
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat ccgacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4956
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4956
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Pro Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4957
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4957
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taatcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4958
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4958
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Asn
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4959
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4959
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gattatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4960
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4960
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4961
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4961
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgagggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4962
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4962
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Glu Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4963
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4963
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagaagg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4964
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4964
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Lys Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4965
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4965
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600

gaaattctgg ataagatgat ttggcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4966
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4966
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Trp
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4967
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4967
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaatc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4968
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4968
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Ser Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4969
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4969
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggg aggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4970
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4970
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Glu Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4971
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4971
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gtcggctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4972
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4972
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4973
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4973
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat tttgcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4974
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4974
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Leu
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4975
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4975
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat gtgacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4976
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4976
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Val Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4977
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4977
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gacggctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4978
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4978
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Thr Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4979
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4979
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaaa ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4980
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4980
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Lys Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4981
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4981
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctcagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4982
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4982
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Gln Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4983
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4983
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4984
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4984
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4985
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4985
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggagacgag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4986
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4986
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Thr Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4987
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4987
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tcgcttggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4988
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4988
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Ala Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4989
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4989
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tgaatgaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4990
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4990
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Asn Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4991
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4991
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt actcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4992
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4992
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4993
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4993
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtg aggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4994
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4994
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Glu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4995
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4995
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctgatggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4996
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4996
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Asp Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4997
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4997
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga ctgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 4998
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4998
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Thr Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 4999
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 4999
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gcgccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5000
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5000
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5001
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5001
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggaggctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5002

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5002
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5003
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5003
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacaatgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5004
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5004
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Asn Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5005
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5005
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat tgagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5006
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5006
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5007

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5007
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaagctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5008
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5008
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5009
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5009
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat gagacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5010
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5010
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Glu Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5011
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5011
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggagaggag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5012
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5012
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Arg Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5013
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5013
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtt ctgaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780

ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5014
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5014
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Ser Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5015
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5015
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac aagccgaaaa ccagccacta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcgcgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accctggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5016
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5016
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Lys Pro Lys Thr Ser His Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Ala
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Leu Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5017
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5017
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5018
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5018
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5019
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5019
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5020
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5020

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5021
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5021
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgcttct 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5022
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5022
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5023
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5023
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacataagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5024
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5024
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5025
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5025

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacataagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5026
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5026
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5027
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5027
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagcttct 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5028
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5028
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5029
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5029
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccaaa gcacgagagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5030
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5030
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5031
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5031
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5032
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5032
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5033
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5033
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccatgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga ccgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5034
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5034
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Thr Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5035
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5035
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgctaaa 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5036
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5036
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5037
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5037
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5038
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5038
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5039
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5039
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgattttgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5040
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5040
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5041
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5041
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5042
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5042
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5043
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5043
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga ccgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5044
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5044
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Thr Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5045
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5045
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5046
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5046
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5047
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5047
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5048
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5048
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5049
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5049
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5050
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5050
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5051
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5051
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacataagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5052
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5052
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5053
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5053
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gcgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5054
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5054
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5055
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5055
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5056
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5056
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5057
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5057
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5058
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5058
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5059
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5059
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagcttct 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5060
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5060
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Met Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5061
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5061
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccatgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5062
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5062
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5063
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5063
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5064
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5064
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5065
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5065
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5066
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5066
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5067
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5067
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagcttct 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5068
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5068
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5069
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5069
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5070
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5070
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5071
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5071
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accataaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgtaccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5072
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5072
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His His Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5073
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5073
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5074
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5074
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5075
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5075
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgctaaa 600

gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5076
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5076
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5077
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5077
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5078
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5078
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5079
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5079
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccatgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaacagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5080
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5080
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5081
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5081
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccatgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga ccgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5082
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5082
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Thr Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5083
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5083
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gatagctaaa 600
gaaattctgg ataagatgat taagcaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgctgc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5084
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5084
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5085
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5085
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggacgctaaa 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacatgagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5086
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5086
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Met Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5087
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5087
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgatgc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5088
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5088
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Met Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5089
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5089
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgcgga ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5090
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5090
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Arg Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5091
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5091
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gactgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5092
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5092
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Thr Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5093
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5093
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggaga gtgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5094
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5094
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5095
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5095
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gtgtgttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5096
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5096
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Cys Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5097
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5097
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaac cgagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5098
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5098
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Pro Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5099
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5099
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5100
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5100
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5101
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5101
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa cctggcttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5102
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5102
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Trp Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5103
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5103
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgtgta ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagtctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5104
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5104
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Cys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5105
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5105
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgctta ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5106
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5106
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Leu Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5107
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5107
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgtattc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5108
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5108
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Tyr
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5109
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5109
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtt gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5110
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5110
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5111
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5111
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccggtga ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5112

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5112
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Val Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5113
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5113
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
gtggaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5114
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5114
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Val Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5115
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5115
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccggc tcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5116
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5116
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Ala His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5117

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5117
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccacgcttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5118
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5118
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Thr Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5119
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5119
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caacgtgtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5120
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5120
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Arg Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5121
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5121
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgatgtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5122
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5122
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Met
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5123
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5123
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaag tgagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780

ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5124
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5124
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Val Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5125
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5125
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc tatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5126
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5126
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5127
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5127
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgcagagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5128
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5128
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Gln Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5129
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5129
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ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagcg ggagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5130
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5130

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Gly Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5131
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5131
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacacggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5132
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5132
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Thr Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5133
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5133
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt tcgcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5134
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5134
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Ser Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5135
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5135

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcggagagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5136
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5136
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5137
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5137
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ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5138
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5138
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5139
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5139
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtatc agaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5140
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5140
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Gln Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5141
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5141
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaaca ttctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5142
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5142
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Ile Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5143
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5143
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcac gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5144
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5144
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Thr Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5145
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5145
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcggta gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5146
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5146
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Gly Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5147
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5147
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctg tatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5148
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5148
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Cys Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5149
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5149
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagatgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5150
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5150
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Met Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5151
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5151
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcaggtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5152
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5152
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Gln Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5153
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5153
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgc gctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5154
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5154
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Ala Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5155
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5155
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggtct gctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5156
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5156
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Leu Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5157
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5157
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agttttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5158
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5158
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5159
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5159
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgta tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5160
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5160
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Met Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5161
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5161
atggagaaca aaaccgaaac cgatgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5162
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5162
Met Glu Asn Lys Thr Glu Thr Asp Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5163
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5163
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt gagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5164
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5164
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Glu Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5165
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5165
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtgc ttgttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5166
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5166
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Leu Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5167
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5167
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtacggtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5168
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5168
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Thr Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5169
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5169
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat ggtggatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5170
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5170
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Val Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5171
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5171
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagacgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5172
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5172
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Thr Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5173
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5173
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg gggccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5174
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5174
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Gly Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5175
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5175
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagtttct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5176
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5176
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Phe Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5177
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5177
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gatactgcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5178
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5178
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Thr
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5179
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5179
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcccta gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5180
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5180
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Pro Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5181
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5181
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
atggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg cctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5182
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5182
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Met Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5183
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5183
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgcgt gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5184
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5184
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Arg Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5185
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5185
atggagaaca aaaccgaaac caccggtcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600

gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5186
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5186
Met Glu Asn Lys Thr Glu Thr Thr Gly Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5187
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5187
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca tgagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5188
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5188
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Met Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5189
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5189
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcggcgagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5190
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5190
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ala Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5191
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5191
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagcgtctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5192
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5192
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Arg Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5193
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5193
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc gaagccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5194
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5194
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Lys Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5195
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5195
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gatccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5196
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5196
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Asp Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5197
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5197
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcgatct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5198
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5198
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Asp
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5199
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5199
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcacgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5200
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5200
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Thr
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5201
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5201
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gtgtcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5202
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5202
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Cys Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5203
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5203
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg tgtccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5204
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5204
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Cys Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5205
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5205
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagctggct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5206
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5206
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Trp
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5207
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5207
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc atgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgc tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5208
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5208
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp His Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Ala Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5209
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5209
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagcc ctagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5210
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5210
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Pro Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5211
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5211
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacttctg gttagctata ttagcagcct g 1371

<210> 5212
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5212
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Leu Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5213
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5213
atggagaaca aaaccgaaac cctggtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5214
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5214
Met Glu Asn Lys Thr Glu Thr Leu Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5215
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5215
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcatgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5216
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5216
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg His Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5217
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5217
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gacggatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5218
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5218
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Thr Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5219
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5219
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caactctccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5220
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5220
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ser Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5221
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5221
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgagtacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5222

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5222
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Ser Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5223
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5223
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
actattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgtt ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5224
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5224
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Thr Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5225
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5225
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg cggattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5226
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5226
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Arg Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5227

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5227
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgataag caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5228
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5228
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Lys Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5229
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5229
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacacgccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5230
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5230
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Thr Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5231
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5231
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtcg tcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5232
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5232
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Arg Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5233
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5233
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg actattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780

ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5234
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5234
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Thr Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5235
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5235
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctggtgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5236
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5236
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Val Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5237
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5237
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacaatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5238
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5238
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asn Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5239
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5239
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gcagcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5240
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5240

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Gln Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5241
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5241
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg cagattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5242
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5242
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Gln Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5243
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5243
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5244
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5244
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5245
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5245

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggactctt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5246
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5246
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Ser Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5247
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5247
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcagg cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5248
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5248
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5249
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5249
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacagtc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840

ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5250
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5250
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ser Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5251
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5251
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
cctattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5252
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5252
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Pro Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5253
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5253
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgggtacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5254
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5254
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Gly Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5255
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5255
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgttgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtct gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5256
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5256
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Leu Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5257
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5257
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caaccagccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5258
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5258
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Gln Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5259
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5259
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg atccgatgat taagcagacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacgagagg gcgagcagca gcagcctgct ggaccacgat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttagcttt 840
ggcacccaga gcgaggtgga cgaaaaggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc tgttccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5260
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5260
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Pro Met Ile Lys
195 200 205
Gln Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Glu Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp His Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Ser Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5261
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5261
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggct agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggaggctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttgga gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5262
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5262
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5263
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5263
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggct agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc aagaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5264
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5264
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Gln Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5265
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5265
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt acgcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5266
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5266
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5267
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5267
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggtccgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5268
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5268
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5269
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5269
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5270
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5270
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5271
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5271
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttgga cggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5272
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5272
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Thr Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5273
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5273
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5274
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5274
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5275
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5275
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggaggcttcc 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5276
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5276
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5277
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5277
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5278
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5278
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5279
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5279
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggct agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5280
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5280
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5281
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5281
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggct agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgcttcc 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5282
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5282
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5283
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5283
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5284
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5284
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5285
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5285
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacaatgat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5286
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5286
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Asn Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5287
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5287
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga cggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacaatgat 780
ccgagcgtgt tcgcctggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5288
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5288
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Thr Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Asn Asp Pro Ser Val Phe Ala Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5289
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5289
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5290
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5290
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5291
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5291
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tcgcctggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5292
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5292
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Ala Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5293
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5293
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggaggctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt acgcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5294
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5294
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5295
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5295
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600

gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacaatgat 780
ccgagcgtgt tcgcctggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt acgcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5296
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5296
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Asn Asp Pro Ser Val Phe Ala Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5297
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5297
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggaggcttcc 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5298
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5298
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5299
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5299
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gagcgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5300
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5300
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5301
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5301
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5302
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5302
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5303
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5303
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggg aagaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5304
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5304
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Glu Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5305
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5305
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gagcgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5306
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5306
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ser Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5307
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5307
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgcttcc 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggg aagaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5308
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5308
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Ser Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Glu Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5309
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5309
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5310
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5310
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5311
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5311
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tgaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5312
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5312
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5313
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5313
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat gagacccgtc ttgaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tgaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5314
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5314
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Glu Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5315
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5315
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat ccaacccgtc ttgaggaacc tgtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5316
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5316
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Pro Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5317
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5317
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aagacccgtg aggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5318
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5318
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Glu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5319
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5319
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat ccaacccgtg agaacgaacc tgtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat ttgggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctgatggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5320
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5320
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Pro Thr Arg Glu Asn Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Trp
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Asp Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5321
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5321
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gtcagctata ttagcagcct g 1371

<210> 5322
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5322
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5323
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5323
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5324
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5324
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5325
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5325
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aagacccgtg agaacgaacc tgtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tgaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5326
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5326
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Glu Asn Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5327
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5327
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat gagacccgtc ttgaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tgaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5328
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5328
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Glu Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5329
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5329
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat gagacccgtc ttgaggaacc tgtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggagacgag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctgatggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5330
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5330
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Glu Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Thr Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Asp Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5331
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5331
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat ccaacccgtc ttaacgaacc tgtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tttggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5332

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5332
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Pro Thr Arg Leu Asn Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Leu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5333
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5333
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tgaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5334
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5334
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5335
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5335
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat gagacccgtc ttgaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tgaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5336
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5336
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Glu Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5337

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5337
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aagacccgtg agaacgaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5338
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5338
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Glu Asn Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5339
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5339
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tgaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5340
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5340
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5341
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5341
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gcgtatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggcg agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcaattt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca gattgctaag 600
gaaattctgg ataagatgat tttggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggagag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacggagat 780
ccgagcgtgt tccagtggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa tgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cgtcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5342
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5342
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Ala Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Leu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Gly Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Cys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5343
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5343
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaga cgagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5344
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5344
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5345
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5345
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaggg tgacccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgaat ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccactcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaag 600
ccgattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5346
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5346
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Arg Val Thr Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ser Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5347
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5347
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5348
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5348
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5349
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5349
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccggtca cgagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgaat ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat cctacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaaaggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5350
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5350

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Val Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Pro Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5351
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5351
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaga cgagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg accattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaag 600
ccgattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctgatggt 1320
ggcagcagcc acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5352
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5352
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Thr Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Asp Gly Gly Ser Ser His Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5353
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5353
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaag 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
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agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt actgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctgatggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5354
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5354
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Leu Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Asp Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5355
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5355

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaga cgagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggactcgt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaag 600
ccgattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaaaggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5356
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5356
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Ser Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5357
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5357
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccggtcg tgagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5358
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5358
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Val Val Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5359
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5359
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccggc tcacattagg gcggaaagca tgagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5360
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5360
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Ala His Ile Arg Ala Glu Ser Met Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5361
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5361
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtt acacattagg gcggaaagct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5362
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5362
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu His Ile Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5363
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5363
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5364
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5364
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5365
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5365
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtcgggct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5366
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5366
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5367
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5367
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacattagg gcggaaggca tgagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5368
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5368
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Glu Gly Met Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5369
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5369
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca tgagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5370
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5370
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Met Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5371
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5371
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5372
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5372
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5373
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5373
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5374
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5374
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5375
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5375
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat ttgggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca tgagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5376
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5376
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Trp
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Met Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5377
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5377
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc aatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccggc tcacattagg gcggaaagca tgagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5378
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5378
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Ala His Ile Arg Ala Glu Ser Met Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5379
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5379
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc aatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taatgaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5380
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5380
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Asn
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5381
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5381
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc aatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5382
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5382
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5383
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5383
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taatgaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtt acactatagg gcggaaagct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5384
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5384
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Asn
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5385
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5385
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtt acactatagg gcggaaggct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5386
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5386
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5387
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5387
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtcgagct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5388
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5388
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5389
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5389
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5390
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5390
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5391
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5391
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taatgaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggtgctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5392
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5392
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Asn
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5393
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5393
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc aatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccggc tcactatagg gcggaaagct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5394
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5394
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Ala His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5395
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5395
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcac aatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taatgaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca tgagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5396
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5396
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Thr Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Asn
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Met Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5397
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5397
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcac aatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtcgagct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5398
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5398
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Thr Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5399
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5399
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5400
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5400
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5401
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5401
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc aatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccggc tcactatagg gcgtcgagct caagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5402
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5402
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Ala His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5403
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5403
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacattagg gcggaaagca tgagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5404
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5404
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Glu Ser Met Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5405
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5405
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600

gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5406
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5406
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5407
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5407
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaacatcgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5408
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5408
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys His Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5409
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5409
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atcggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5410
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5410
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5411
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5411
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgct tgttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5412
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5412
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Leu Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5413
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5413
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcatgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5414
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5414
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala His Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5415
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5415
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaatcggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5416
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5416
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Ser Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5417
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5417
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc tgtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5418
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5418
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5419
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5419
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgta ctgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5420
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5420
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Thr Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5421
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5421
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct gcagaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5422
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5422
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Gln Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5423
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5423
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gagaaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5424
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5424
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Glu Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5425
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5425
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggagctgaag gataaagcga atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5426
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5426
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Glu Leu Lys Asp Lys
420 425 430
Ala Asn Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5427
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5427
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaag ctagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5428
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5428
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Ala Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5429
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5429
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat acgacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5430
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5430
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Thr Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5431
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5431
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5432
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5432
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5433
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5433
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag cgtaaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5434
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5434
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Arg Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5435
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5435
atgcttaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5436
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5436
Met Leu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5437
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5437
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5438
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5438
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5439
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5439
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtt ggaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5440
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5440
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Trp Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5441
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5441
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaacgct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5442

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5442
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Thr Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5443
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5443
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgcttgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5444
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5444
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Leu Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5445
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5445
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5446
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5446
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5447

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5447
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5448
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5448
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5449
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5449
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgtgtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5450
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5450
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Cys Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5451
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5451
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggcgggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5452
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5452
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Ala Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5453
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5453
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg tgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5454
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5454
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5455
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5455
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gattctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5456
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5456
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Ile Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5457
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5457
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatgc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5458
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5458
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Met Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5459
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5459
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg cttagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5460
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5460

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Leu Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5461
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5461
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg ataagagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5462
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5462
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Lys Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5463
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5463
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5464
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5464
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5465
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5465

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgtc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5466
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5466
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Cys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5467
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5467
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccacacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacca tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5468
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5468
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His His Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5469
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5469
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat tcgacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5470
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5470
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Ser Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5471
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5471
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcaggg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5472
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5472
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Gln Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5473
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5473
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
ttcaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttggg 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5474
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5474
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gly Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5475
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5475
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccggtggat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5476
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5476
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Val Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5477
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5477
atgaataaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5478
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5478
Met Asn Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5479
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5479
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atatgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5480
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5480
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Met Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5481
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5481
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgcaggat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa acactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5482
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5482
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gln Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5483
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5483
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgcctagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5484
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5484
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5485
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5485
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatccgttc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5486
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5486
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Pro Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5487
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5487
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgttgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gtcgctgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5488
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5488
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Ser Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5489
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5489
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtgtcgggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5490
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5490
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5491
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5491
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcaccc tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5492
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5492
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Pro Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5493
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5493
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcggcggg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5494
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5494
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Ala Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5495
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5495
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtg ctaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5496
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5496
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Ala Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5497
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5497
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttgtgc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5498
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5498
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Val Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5499
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5499
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccggaggat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5500
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5500
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5501
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5501
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atacgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5502
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5502
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Thr Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5503
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5503
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttgcggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5504
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5504
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Ala Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5505
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5505
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaggctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5506
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5506
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Arg Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5507
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5507
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gcagctgaag gataaagcgg atgtgagcct ggctaaggggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5508
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5508
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Gln Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5509
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5509
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttttgc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5510
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5510
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Leu Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5511
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5511
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgctgttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5512
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5512
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Leu Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5513
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5513
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gtttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5514
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5514
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Phe Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5515
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5515
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag ccagggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600

gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5516
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5516
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Gln Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5517
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5517
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cgcaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5518
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5518
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5519
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5519
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacag ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5520
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5520
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Arg Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5521
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5521
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg ataattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgtctgat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5522
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5522
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Ser Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5523
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5523
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaaatcgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5524
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5524
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Asn Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5525
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5525
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg attgtagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5526
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5526
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Cys Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5527
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5527
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat gtgacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5528
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5528
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Val Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5529
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5529
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg tgttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5530
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5530
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5531
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5531
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ctatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5532
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5532
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Ser
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5533
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5533
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cacgtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5534
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5534
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5535
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5535
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttgggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5536
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5536
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gly Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5537
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5537
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacactgat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5538
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5538
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5539
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5539
atggagaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5540
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5540
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5541
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5541
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatcaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
acctttcgtt ttatcttgga caaggatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaag cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc ggttctgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5542
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5542
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Thr Phe Arg Phe
50 55 60
Ile Leu Asp Lys Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Val Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5543
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5543
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacataagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5544
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5544
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5545
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5545
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacataagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5546
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5546
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5547
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5547
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaagccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcacataagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5548
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5548
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ile Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5549
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5549
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5550
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5550
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5551
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5551
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca gatagccaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5552

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5552
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5553
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5553
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaaaaaaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5554
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5554
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5555
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5555
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaagccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5556
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5556
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5557

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5557
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5558
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5558
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5559
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5559
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5560
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5560
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5561
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5561
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5562
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5562
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5563
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5563
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5564
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5564
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5565
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5565
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5566
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5566
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5567
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5567
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca gatagccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5568
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5568
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5569
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5569
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgc ccaggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5570
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5570

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5571
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5571
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5572
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5572
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5573
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5573
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaagccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaaggggag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5574
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5574
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5575
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5575

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5576
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5576
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5577
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5577
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaagccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5578
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5578
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5579
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5579
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5580
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5580
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5581
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5581
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5582
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5582
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5583
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5583
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5584
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5584
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5585
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5585
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5586
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5586
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5587
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5587
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5588
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5588
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5589
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5589
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaagccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5590
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5590
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5591
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5591
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgccaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5592
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5592
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5593
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5593
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggataaaaaa 600
gaaattctgg ataagatgat taaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5594
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5594
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Lys Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5595
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5595
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggataaaaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5596
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5596
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Lys Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5597
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5597
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaagccaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5598
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5598
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5599
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5599
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5600
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5600
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5601
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5601
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5602
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5602
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5603
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5603
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgaaaagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaaggggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5604
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5604
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Lys
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5605
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5605
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggggcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5606
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5606
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Gly Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5607
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5607
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggataacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5608
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5608
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5609
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5609
atgcacaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5610
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5610
Met His Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5611
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5611
atgggcaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5612
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5612
Met Gly Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5613
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5613
atgccgaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5614
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5614
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5615
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5615
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttc gtgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5616
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5616
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Arg Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5617
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5617
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acgcgctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5618
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5618
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ala Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5619
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5619
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat acaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5620
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5620
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Thr Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5621
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5621
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagcc ttggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5622
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5622
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Leu Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5623
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5623
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaaccaatc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5624
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5624
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Asn Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5625
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5625
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600

gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcccccc ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5626
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5626
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Pro

245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5627
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5627
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcac tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5628
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5628
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Thr Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5629
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5629
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca agacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5630
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5630
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5631
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5631
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5632
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5632
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5633
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5633
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttcgggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaaggg 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5634
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5634
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5635
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5635
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcga gcagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5636
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5636
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Ser Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5637
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5637
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aggatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5638
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5638
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5639
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5639
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga agatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5640
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5640
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asp Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5641
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5641
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggagaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5642
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5642
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Glu Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5643
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5643
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5644
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5644
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5645
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5645
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctggacgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5646
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5646
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Asp Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5647
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5647
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagcagga ttagcagcct g 1371

<210> 5648
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5648
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Arg Ile Ser Ser Leu
450 455

<210> 5649
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5649
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctgcgggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5650
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5650
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Ala Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5651
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5651
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5652
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5652
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5653
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5653
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agccggcaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5654
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5654
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5655
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5655
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctggc tgacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5656
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5656
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5657
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5657
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcatgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5658
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5658
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg His Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5659
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5659
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgac cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5660
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5660
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5661
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5661
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccctc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5662

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5662
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Pro Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5663
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5663
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5664
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5664
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5665
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5665
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga ttgtattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5666
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5666
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Cys Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5667

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5667
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg ggagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5668
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5668
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Gly Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5669
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5669
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaactgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5670
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5670
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Thr Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5671
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5671
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcggga gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5672
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5672
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5673
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5673
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttggg 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5674
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5674
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Gly Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5675
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5675
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggaccctt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5676
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5676
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Pro Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5677
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5677
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacgctaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5678
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5678
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Ala Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5679
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5679
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct gcaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5680
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5680

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu His Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5681
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5681
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggcgcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5682
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5682
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Ala Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5683
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5683
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acacgagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5684
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5684
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Thr Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5685
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5685

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacacct ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5686
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5686
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Thr Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5687
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5687
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt caacgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5688
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5688
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5689
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5689
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gataatcccg atcattaacg agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaacttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaaca agtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat taaggaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcgt ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5690
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5690
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Ile Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Asn Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Gln Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Lys
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5691
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5691
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ctatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcaccc tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5692
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5692
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Ser
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Pro Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5693
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5693
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggagat acaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5694
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5694
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Thr Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5695
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5695
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat acacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gagattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcaaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5696
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5696
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Thr His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5697
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5697
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5698
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5698
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5699
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5699
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg accattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggagat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5700
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5700
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Thr Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5701
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5701
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5702
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5702
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5703
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5703
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat acaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcaaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5704
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5704
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Thr Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5705
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5705
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcaccc tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcaaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5706
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5706
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Pro Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5707
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5707
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5708
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5708
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5709
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5709
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggagat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5710
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5710
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5711
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5711
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5712
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5712
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5713
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5713
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ctatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gagattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggtccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcaccc tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5714
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5714
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Ser
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Val Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Pro Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5715
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5715
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggagat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5716
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5716
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5717
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5717
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg accattaacg aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggagat acacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5718
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5718
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Thr Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Thr His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5719
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5719
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggagat acacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5720
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5720
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Thr His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5721
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5721
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaacg aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcaaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5722
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5722
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Gln Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5723
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5723
atggagaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaaggggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5724
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5724
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5725
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5725
atggaaaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5726
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5726
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5727
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5727
atggaaaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5728
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5728
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5729
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5729
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5730
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5730
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5731
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5731
atggaaaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5732
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5732
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5733
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5733
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgc ccaggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5734
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5734
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5735
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5735
atggagaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600

gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg cagactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5736
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5736
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Arg Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5737
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5737
atggagaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5738
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5738
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5739
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5739
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc cagactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5740
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5740
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Arg Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5741
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5741
atggaaaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5742
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5742
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5743
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5743
atggaaaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgct caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5744
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5744
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Leu Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5745
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5745
atggaaaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgct caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5746
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5746
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Leu Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5747
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5747
atggaaaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgct caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5748
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5748
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Leu Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5749
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5749
atggagaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5750
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5750
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5751
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5751
atggagaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5752
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5752
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5753
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5753
atggaaaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgct caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5754
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5754
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Leu Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5755
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5755
atgaataaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5756
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5756
Met Asn Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5757
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5757
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc cagactgaag gataaagcgg atgtgagcct ggctaaggggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5758
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5758
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Arg Leu Lys Asp Lys

420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5759
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5759
atgctgaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg cagactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5760
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5760
Met Leu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Arg Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5761
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5761
atggagaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg cagactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5762
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5762
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Arg Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5763
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5763
atggaaaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc cagactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5764
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5764
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Arg Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5765
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5765
atgaataaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5766
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5766
Met Asn Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5767
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5767
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5768
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5768
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5769
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5769
atggaaaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5770
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5770
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5771
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5771
atggagaaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg caaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5772

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5772
Met Glu Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5773
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5773
atggagaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaaggg 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5774
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5774
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5775
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5775
atggagaaca aaaccgaaac gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaatgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5776
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5776
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5777

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5777
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagctt gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5778
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5778
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5779
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5779
atgaataaca aaaccgaacc gaccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaggca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga acgggcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc cagactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5780
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5780
Met Asn Asn Lys Thr Glu Pro Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Gly Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Arg Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Arg Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5781
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5781
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggctcacga ttcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttc gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggaaaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg ataggagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5782
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5782
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ser Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Arg Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5783
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5783
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttc gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaaggggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5784
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5784
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Arg Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5785
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5785
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagcgctta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5786
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5786
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Ala Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5787
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5787
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccgttcttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5788
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5788
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Val Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5789
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5789
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcaggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5790
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5790

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Gln Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5791
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5791
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgcagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5792
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5792
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Gln
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5793
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5793
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg cggtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5794
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5794
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5795
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5795

atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5796
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5796
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5797
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5797
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggctctcaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5798
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5798
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5799
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5799
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gttggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5800
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5800
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5801
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5801
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gtgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5802
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5802
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5803
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5803
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatctg taacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5804
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5804
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Cys Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5805
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5805
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt tgtaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5806
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5806
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Cys Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5807
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5807
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt taacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5808
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5808
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5809
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5809
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5810
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5810
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5811
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5811
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcctgctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5812
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5812
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Leu Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5813
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5813
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagagcttg gctacctgga tccgggtgat aaaacccgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
gaaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgt tccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacga tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgaaagtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgcagcgtc aaaacgcggc gaaactgaag gataaagcgg atgtgagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5814
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5814
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Gly Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Glu Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Phe Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Asp Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Gln Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Val Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5815
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5815
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttt ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5816
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5816
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5817
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5817
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5818
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5818
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5819
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5819
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5820
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5820
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5821
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5821
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtccagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5822
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5822
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5823
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5823
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5824
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5824
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5825
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5825
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gccaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttt ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5826
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5826
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Gln Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5827
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5827
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcactcaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5828
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5828
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5829
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5829
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gccaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5830
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5830
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Gln Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5831
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5831
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct gcatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttt ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5832
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5832
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu His Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5833
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5833
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtccagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5834
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5834
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5835
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5835
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5836
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5836
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5837
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5837
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttt ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5838
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5838
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5839
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5839
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5840
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5840
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5841
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5841
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcct tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5842
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5842
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5843
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5843
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5844
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5844
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5845
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5845
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttt ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5846
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5846
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5847
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5847
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5848
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5848
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5849
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5849
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5850
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5850
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5851
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5851
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtccagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5852
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5852
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5853
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5853
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtccagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5854
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5854
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5855
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5855
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5856
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5856
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5857
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5857
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttt ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5858
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5858
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5859
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5859
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5860
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5860
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5861
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5861
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacgg cgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5862
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5862
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255

Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5863
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5863
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gccaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcct tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5864
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5864
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Gln Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5865
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5865
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5866
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5866
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5867
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5867
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5868
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5868
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5869
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5869
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5870
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5870
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5871
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5871
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtccagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgttg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5872
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5872
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5873
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5873
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5874
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5874
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5875
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5875
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5876
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5876
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5877
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5877
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5878
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5878
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5879
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5879
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5880
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5880
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5881
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5881
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtccagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cagcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5882

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5882
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Gln Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5883
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5883
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5884
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5884
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5885
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5885
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcgt tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5886
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5886
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Val Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5887

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5887
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatctttt ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5888
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5888
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5889
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5889
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataacc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgtccagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta aagatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5890
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5890
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Asn Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Lys Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5891
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5891
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcgcg gaaactgaag gataaagcgg atcgaagcct tgctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5892
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5892
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5893
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5893
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctggc agacgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5894
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5894
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Ala Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5895
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5895
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatagac tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcggaaagca gcagcctgct agacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gccaagtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt cggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5896
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5896
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Lys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Glu Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Gln Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5897
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5897
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5898
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5898
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5899
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5899
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5900
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5900

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5901
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5901
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5902
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5902
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5903
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5903
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5904
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5904
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5905
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5905

atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagccgaa ttagcagcct g 1371

<210> 5906
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5906
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Arg Ile Ser Ser Leu
450 455

<210> 5907
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5907
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5908
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5908
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5909
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5909
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5910
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5910
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5911
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5911
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagccgaa ttagcagcct g 1371

<210> 5912
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5912
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Arg Ile Ser Ser Leu
450 455

<210> 5913
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5913
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5914
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5914
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5915
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5915
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagagctag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5916
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5916
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5917
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5917
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5918
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5918
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5919
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5919
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagctag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5920
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5920
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5921
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5921
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5922
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5922
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5923
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5923
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5924
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5924
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5925
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5925
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5926
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5926
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5927
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5927
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5928
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5928
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5929
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5929
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5930
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5930
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5931
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5931
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5932
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5932
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 5933
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5933
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5934
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5934
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5935
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5935
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5936
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5936
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5937
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5937
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagagctag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5938
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5938
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5939
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5939
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagctag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5940
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5940
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5941
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5941
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5942
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5942
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5943
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5943
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5944
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5944
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5945
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5945
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5946
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5946
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5947
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5947
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5948
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5948
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5949
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5949
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5950
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5950
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5951
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5951
atggagaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5952
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5952
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5953
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5953
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5954
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5954
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5955
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5955
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagagctag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttagagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5956
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5956
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5957
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5957
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5958
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5958
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5959
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5959
atgcccaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5960
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5960
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5961
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5961
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5962
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5962
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5963
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5963
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagagcgag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcagacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctaca ttagcagcct g 1371

<210> 5964
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5964
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Arg Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Arg Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5965
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5965
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5966
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5966
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5967
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5967
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccacagttt 480
ttagagctag gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5968
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5968
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5969
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5969
atgcccaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccgtcag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5970
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5970
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5971
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5971
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggaccagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggaga gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctaca ttagcagcct g 1371

<210> 5972
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5972
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ser Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5973
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5973
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgt cctcgctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgcccagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5974
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5974
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Ser Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5975
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5975
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5976
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5976
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5977
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5977
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgaagagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcaattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5978
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5978
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Lys
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5979
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5979
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgt ccgcgctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggctcagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5980
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5980
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Ser Ala Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Ala Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5981
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5981
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcaattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5982
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5982
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5983
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5983
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgaagagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5984
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5984
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Lys
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5985
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5985
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgcccagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta ccgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5986
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5986
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Thr Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5987
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5987
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgt ccgcgctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgcccagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcatgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5988
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5988
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Ser Ala Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg His Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5989
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5989
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggctcagcaa ccgcccagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5990
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5990
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Ala Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5991
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5991
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggatcagcaa ccgcccagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga agacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5992

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5992
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asp Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5993
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5993
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggctcagcaa ccgcccagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcaattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5994
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5994
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Ala Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5995
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5995
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaattgct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5996
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5996
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Leu Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5997

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5997
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaggctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 5998
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5998
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 5999
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 5999
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaggctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcccggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6000
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6000
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Pro Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6001
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6001
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaaca agctcggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaggctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6002
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6002
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Lys Leu Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6003
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6003
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca gattgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6004
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6004
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6005
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6005
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagtcgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6006
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6006
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6007
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6007
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca gattgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc tgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6008
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6008
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Leu Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6009
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6009
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6010
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6010

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6011
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6011
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca ggaggctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6012
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6012
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6013
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6013
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggttg gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct tatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gcaattggca gattgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccg tgaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctaagggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6014
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6014
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Trp Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser Asn Trp Gln Ile Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Arg Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6015
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6015

atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6016
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6016
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6017
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6017
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6018
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6018
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6019
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6019
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6020
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6020
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6021
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6021
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6022
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6022
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6023
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6023
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6024
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6024
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6025
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6025
atggagaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6026
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6026
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6027
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6027
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6028
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6028
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6029
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6029
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6030
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6030
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6031
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6031
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6032
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6032
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6033
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6033
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa actgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6034
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6034
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6035
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6035
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6036
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6036
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6037
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6037
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6038
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6038
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6039
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6039
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6040
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6040
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6041
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6041
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6042
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6042
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6043
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6043
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6044
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6044
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6045
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6045
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6046
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6046
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6047
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6047
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6048
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6048
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6049
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6049
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6050
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6050
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6051
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6051
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6052
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6052
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6053
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6053
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6054
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6054
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6055
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6055
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt tgtcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6056
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6056
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Cys His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6057
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6057
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6058
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6058
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6059
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6059
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6060
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6060
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6061
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6061
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6062
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6062
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6063
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6063
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6064
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6064
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6065
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6065
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6066
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6066
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6067
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6067
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6068
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6068
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6069
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6069
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6070
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6070
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6071
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6071
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6072
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6072
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6073
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6073
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6074
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6074
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6075
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6075
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6076
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6076
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6077
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6077
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6078
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6078
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6079
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6079
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6080
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6080
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6081
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6081
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttcca 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6082
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6082
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6083
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6083
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6084
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6084
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6085
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6085
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6086
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6086
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6087
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6087
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6088
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6088
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6089
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6089
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6090
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6090
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6091
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6091
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6092
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6092
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6093
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6093
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttcca 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt tgtcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6094
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6094
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Cys His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6095
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6095
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt tgtcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6096
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6096
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Cys His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6097
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6097
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6098
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6098
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6099
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6099
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6100
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6100
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6101
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6101
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6102

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6102
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6103
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6103
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6104
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6104
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6105
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6105
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6106
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6106
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6107

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6107
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6108
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6108
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6109
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6109
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt tgtcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6110
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6110
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Cys His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6111
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6111
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6112
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6112
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6113
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6113
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6114
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6114
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6115
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6115
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6116
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6116
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6117
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6117
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6118
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6118
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6119
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6119
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6120
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6120

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6121
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6121
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt tgtcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6122
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6122
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Cys His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6123
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6123
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6124
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6124
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6125
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6125

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6126
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6126
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6127
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6127
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6128
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6128
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6129
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6129
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6130
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6130
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6131
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6131
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6132
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6132
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6133
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6133
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6134
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6134
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6135
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6135
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6136
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6136
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6137
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6137
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6138
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6138
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6139
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6139
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6140
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6140
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6141
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6141
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6142
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6142
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6143
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6143
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6144
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6144
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6145
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6145
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6146
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6146
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6147
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6147
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6148
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6148
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6149
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6149
atgccaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6150
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6150
Met Pro Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6151
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6151
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6152
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6152
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6153
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6153
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6154
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6154
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6155
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6155
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6156
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6156
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6157
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6157
atggaaaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6158
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6158
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6159
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6159
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6160
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6160
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6161
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6161
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6162
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6162
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6163
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6163
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6164
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6164
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6165
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6165
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6166
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6166
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6167
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6167
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt tgtcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6168
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6168
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Cys His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6169
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6169
atggaaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggaggacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6170
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6170
Met Glu Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asp Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6171
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6171
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggggtcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6172
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6172
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Gly Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6173
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6173
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgagtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6174
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6174
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Ser Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6175
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6175
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttctgcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6176
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6176
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6177
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6177
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa gtggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6178
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6178
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Val Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6179
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6179
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tgtgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6180
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6180
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Val Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6181
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6181
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcagt atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6182
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6182
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Ser Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6183
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6183
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagcc agagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6184
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6184
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Gln Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6185
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6185
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgcgtcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6186
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6186
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6187
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6187
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gcatcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6188
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6188
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala His Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6189
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6189
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaatatgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6190
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6190
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Tyr Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6191
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6191
atggagaaca aaaccgaaac caccgtgcgt cgttcgcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6192
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6192
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Ser Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6193
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6193
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcacg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6194
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6194
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Thr Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6195
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6195
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggtttcgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6196
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6196
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Ser
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6197
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6197
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctggctcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6198
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6198
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Ala Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6199
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6199
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgaa gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6200
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6200
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Lys Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6201
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6201
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcaccg tgtttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6202
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6202
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Val Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6203
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6203
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6204
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6204
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6205
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6205
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg gagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6206
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6206
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6207
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6207
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgtg tcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6208
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6208
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6209
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6209
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct gaatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6210
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6210
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asn Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6211
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6211
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag accgtgaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6212

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6212
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Arg Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6213
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6213
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa aagggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6214
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6214
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6215
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6215
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggatgcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6216
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6216
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Met Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6217

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6217
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttctgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6218
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6218
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Leu
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6219
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6219
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaac ctgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6220
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6220
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Pro Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6221
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6221
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagctctgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6222
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6222
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ser Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6223
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6223
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagccggct g 1371

<210> 6224
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6224
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Arg Leu
450 455

<210> 6225
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6225
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagctagct g 1371

<210> 6226
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6226
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser
450 455

<210> 6227
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6227
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgtct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6228
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6228
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6229
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6229
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgataag caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6230
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6230
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Lys Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6231
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6231
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgctgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6232
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6232
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6233
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6233
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6234
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6234
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6235
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6235
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6236
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6236
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6237
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6237
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaatggaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6238
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6238
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6239
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6239
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgct gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6240
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6240
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6241
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6241
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaactgg atcgaagcct ggctcccggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6242
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6242
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6243
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6243
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagcgcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gcgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6244
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6244
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Ala Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6245
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6245
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gttgtatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6246
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6246
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Leu Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6247
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6247
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gatcttgcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6248
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6248
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6249
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6249
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtgttatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6250
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6250
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Cys Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6251
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6251
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc ctgaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6252
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6252
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6253
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6253
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcaatgaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6254
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6254
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Asn
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6255
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6255
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6256
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6256
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6257
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6257
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatccag atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6258
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6258
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Gln Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6259
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6259
atggagaaca aaaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagc atcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggatgctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcacccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg gcgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcga aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6260
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6260
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu His Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Asp Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Thr Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Gly Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Glu Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6261
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6261
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6262
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6262
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6263
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6263
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6264
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6264
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6265
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6265
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6266
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6266
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6267
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6267
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6268
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6268
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6269
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6269
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6270
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6270
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6271
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6271
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttcca 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6272
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6272
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6273
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6273
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6274
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6274
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6275
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6275
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6276
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6276
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6277
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6277
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6278
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6278
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6279
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6279
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6280
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6280
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6281
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6281
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6282
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6282
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6283
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6283
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6284
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6284
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6285
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6285
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6286
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6286
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6287
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6287
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6288
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6288
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6289
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6289
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6290
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6290
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6291
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6291
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagctgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6292
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6292
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6293
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6293
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagctgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6294
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6294
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6295
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6295
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6296
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6296
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6297
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6297
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6298
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6298
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6299
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6299
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6300
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6300
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6301
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6301
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6302
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6302
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6303
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6303
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6304
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6304
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6305
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6305
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6306

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6306
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6307
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6307
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6308
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6308
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6309
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6309
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6310
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6310
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6311

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6311
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6312
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6312
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6313
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6313
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6314
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6314
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6315
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6315
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6316
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6316
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6317
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6317
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6318
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6318
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6319
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6319
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6320
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6320
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6321
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6321
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6322
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6322
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6323
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6323
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6324
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6324

Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6325
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6325
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6326
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6326
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6327
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6327
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6328
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6328
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6329
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6329

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6330
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6330
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6331
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6331
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6332
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6332
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6333
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6333
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6334
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6334
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6335
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6335
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagctgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6336
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6336
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6337
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6337
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6338
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6338
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6339
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6339
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtcg cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6340
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6340
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6341
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6341
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggagg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6342
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6342
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6343
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6343
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtcg cgagtggatt 960
gagctgctgc cggatggttt tctgggcgat cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6344
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6344
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Arg Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Asp Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6345
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6345
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgta ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgca ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caatgggtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6346
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6346
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Ile Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Gln Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Trp Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6347
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6347
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagaggctg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6348
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6348
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6349
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6349
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ttcccgggcc accttaaccc gatgatgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gccctttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6350
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6350
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Met Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6351
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6351
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgc atgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6352
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6352
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro His Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6353
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6353
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6354
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6354
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6355
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6355
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgctttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6356
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6356
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Ala Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6357
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6357
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6358
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6358
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6359
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6359
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccacatctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6360
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6360
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6361
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6361
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggttctg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6362
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6362
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Ser Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6363
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6363
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaacgctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6364
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6364
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Thr Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6365
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6365
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccga atgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960

gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6366
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6366
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Asn Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6367
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6367
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcttgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6368
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6368
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Leu Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6369
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6369
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccgcagccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6370
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6370
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Gln Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6371
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6371
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcac tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaaatgaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6372
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6372
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Met Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6373
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6373
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccacagctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6374
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6374
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Gln Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6375
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6375
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctggttg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6376
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6376
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Val Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6377
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6377
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
acgggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6378
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6378
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6379
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6379
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgttttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6380
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6380
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Val Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6381
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6381
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaatataaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6382
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6382
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Tyr Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6383
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6383
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagtctgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6384
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6384
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Ser Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6385
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6385
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6386
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6386
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6387
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6387
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacggagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6388
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6388
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6389
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6389
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtaatg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6390
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6390
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Asn Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6391
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6391
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agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gaagatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
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ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
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agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
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<210> 6392
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6392
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Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Lys Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6393
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

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agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctttcgct ggatcagttt 480
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ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
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ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6394
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6394
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6395
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

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agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
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ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaacataaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
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ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
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<210> 6396
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6396
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Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu His Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

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<211> 1371
<212> DNA
<213> Artificial Sequence

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agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgcct 240
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cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
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ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
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gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
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accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
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gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
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<210> 6398
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6398
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Pro
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val

305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6399
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

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agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg gttgacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6400
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6400
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Val Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6401
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6401
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtgctg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6402
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6402
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Ala Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6403
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6403
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaaacgacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6404
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6404
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Thr Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6405
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6405
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagagaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6406
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6406
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Glu Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6407
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6407
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtacgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6408
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6408
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Thr Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6409
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6409
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccagttctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6410
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6410
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Val Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6411
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6411
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg atgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6412
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6412
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Asp Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6413
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6413
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gtgtatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6414
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6414
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Cys Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320

Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6415
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6415
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaacagaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6416

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6416
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Gln Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6417
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6417
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcacgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6418
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6418
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Thr Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6419
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6419
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat ggcgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6420
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6420
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Ala Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6421

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6421
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtaagg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6422
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6422
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Lys Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6423
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6423
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gcatatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6424
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6424
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met His Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6425
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6425
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6426
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6426
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6427
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6427
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgacgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6428
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6428
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Thr Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6429
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6429
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6430
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6430
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6431
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6431
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggctagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6432
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6432
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Ala Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6433
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6433
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6434
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6434

Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6435
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6435
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcata gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6436
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6436
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
His Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6437
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6437
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6438
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6438
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6439
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6439

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga ttgtgaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6440
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6440
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Cys Glu Asp Lys His Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6441
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6441
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6442
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6442
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6443
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6443
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agaatggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6444
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6444
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys Asn Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6445
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6445
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgagtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6446
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6446
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ser Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6447
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6447
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcgac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6448
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6448
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe Ser Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6449
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6449
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccggcta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6450
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6450
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ala Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6451
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6451
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgctgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6452
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6452
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Leu Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6453
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6453
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6454
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6454
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6455
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6455
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcacagtagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6456
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6456
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Ser Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6457
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6457
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6458
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6458
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6459
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6459
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggaag acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct ggatcagttt 480
ttagagcttg gctacctgga tactgaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggacgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtgggtt 960
gagccgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcct ggctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6460
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6460
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Glu Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Asp Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Val
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6461
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6461
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg tcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaatggaag gataaggccg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6462
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6462
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6463
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6463
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtt gcattatagg gcgagcagct ccagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6464
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6464
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6465
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6465
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtt gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6466
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6466
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6467
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6467
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6468
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6468
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6469
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6469
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg ttggtatagg gcgagcagct ccagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgacca ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6470
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6470
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Gln Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6471
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6471
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaatggaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6472
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6472
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6473
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6473
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggtttcgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6474
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6474
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Ser
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6475
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6475
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960

gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgctgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaatggaag gataaggccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6476
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6476
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6477
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6477
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgctgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6478
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6478
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6479
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6479
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgcagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggtttcgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaatggaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6480
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6480
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Ser

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Trp Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6481
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6481
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgcagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaatggaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6482
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6482
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6483
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6483
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgatgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg ttggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaggccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6484
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6484
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Met Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6485
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6485
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttcttcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6486
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6486
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6487
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6487
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttcttcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttttgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6488
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6488
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Leu
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6489
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6489
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagcc agagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6490
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6490
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Gln Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6491
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6491
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagcc agagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6492
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6492
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Gln Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6493
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6493
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagct ccagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6494
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6494
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6495
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6495
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttagagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6496
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6496
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6497
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6497
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttacttcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttttgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6498
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6498
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Leu
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6499
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6499
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttttgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6500
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6500
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Leu
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6501
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6501
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg tcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6502
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6502
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6503
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6503
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaatggaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6504
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6504
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6505
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6505
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaatggaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6506
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6506
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Trp Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6507
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6507
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6508
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6508
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6509
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6509
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagcc agagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggtttcgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6510
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6510
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Gln Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Ser
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6511
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6511
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgccggaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6512
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6512
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Pro Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu

420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6513
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6513
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6514
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6514
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6515
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6515
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagcc agagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6516
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6516
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Gln Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6517
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6517
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcataacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagct ccagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttccttcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6518
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6518
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6519
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6519
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagct ccagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6520
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6520
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6521
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6521
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6522
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6522
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6523
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6523
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgccggaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6524
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6524
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Pro Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6525
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6525
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgccggaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaatggaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6526

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6526
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Pro Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6527
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6527
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaatggaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6528
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6528
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Leu
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6529
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6529
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttttgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6530
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6530
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Leu
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6531

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6531
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6532
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6532
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6533
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6533
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaatggaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6534
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6534
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6535
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6535
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcatgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6536
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6536
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Met
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6537
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6537
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg ttggtatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6538
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6538
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6539
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6539
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6540
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6540
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6541
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6541
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg tcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6542
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6542
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6543
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6543
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgctgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggtttcgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6544
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6544

Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Ser
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6545
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6545
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgctgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6546
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6546
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6547
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6547
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg ttggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgcagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6548
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6548
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Ala Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6549
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6549

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagcc agagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttagagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6550
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6550
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Gln Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6551
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6551
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6552
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6552
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6553
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6553
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtg tcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6554
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6554
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Cys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6555
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6555
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaggccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6556
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6556
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6557
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6557
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6558
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6558
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6559
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6559
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttttgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6560
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6560
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Leu
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6561
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6561
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagcc agagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6562
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6562
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Gln Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6563
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6563
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6564
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6564
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6565
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6565
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgtt gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6566
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6566
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Leu His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6567
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6567
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaatggaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6568
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6568
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Trp Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6569
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6569
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg ctggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6570
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6570
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Leu Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6571
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6571
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6572
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6572
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6573
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6573
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagcg ccagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6574
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6574
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ala Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6575
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6575
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6576
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6576
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6577
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6577
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6578
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6578
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6579
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6579
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttttgcc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6580
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6580
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Leu
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6581
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6581
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttagccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6582
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6582
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6583
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6583
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaattgaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6584
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6584
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6585
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6585
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960

gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
tttcttcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc aaaatggaag gatttattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6586
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6586
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6587
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6587
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaggccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6588
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6588
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6589
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6589
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtcg gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6590
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6590
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Arg Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6591
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6591
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6592
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6592
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6593
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6593
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6594
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6594
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6595
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6595
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcaggtat gagaatcccg aatattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6596
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6596
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Asn Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6597
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6597
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg actattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6598
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6598
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Thr Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6599
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6599
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acatgaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6600
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6600
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Met Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6601
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6601
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacatgccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6602
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6602
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Met Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6603
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6603
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtca gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6604
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6604
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Gln Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6605
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6605
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6606
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6606
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6607
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6607
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
tgtatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6608
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6608
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Cys Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6609
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6609
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acattaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaat gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6610
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6610
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6611
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6611
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc tagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6612
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6612
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6613
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6613
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtga gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc tgcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6614
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6614
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Glu Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6615
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6615
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgttc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6616
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6616
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Val Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6617
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6617
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacactc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6618
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6618
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Thr Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6619
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6619
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggctt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6620
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6620
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6621
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6621
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acagtaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6622
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6622
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ser Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys

420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6623
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6623
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6624
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6624
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6625
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6625
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg gtgattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6626
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6626
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Val Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6627
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6627
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cttattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6628
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6628
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6629
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6629
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttatgc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6630
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6630
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Met Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6631
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6631
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6632
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6632
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6633
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6633
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttgtgc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6634
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6634
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Val Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6635
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6635
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctaa tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttcgc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6636

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6636
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ser Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6637
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6637
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtcttagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6638
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6638
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430

Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6639
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6639
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcttc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6640
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6640
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Leu Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6641

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6641
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6642
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6642
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6643
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6643
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
attatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6644
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6644
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Ile Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6645
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6645
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgtc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6646
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6646
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Cys Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6647
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6647
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcagc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6648
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6648
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6649
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6649
atgccaaaca caaccccgac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6650
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6650
Met Pro Asn Thr Thr Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6651
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6651
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcaccc tgcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6652
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6652
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Pro Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6653
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6653
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaggttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6654
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6654

Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Arg Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6655
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6655
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgaagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6656
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6656
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6657
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6657
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccctaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6658
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6658
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6659
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6659

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaatctcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6660
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6660
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys Ser Arg Leu Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6661
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6661
atgccaaaca catcggaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6662
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6662
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6663
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6663
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttggtc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6664
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6664
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gly Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6665
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6665
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaatgta gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6666
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6666
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Cys Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6667
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6667
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttgctc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6668
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6668
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ala Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6669
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6669
atgccaaaca caaccgaaac caccgtgaag cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6670
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6670
Met Pro Asn Thr Thr Glu Thr Thr Val Lys Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6671
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6671
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttaggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6672
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6672
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Arg Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6673
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6673
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaaactcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6674
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6674
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys Thr Arg Leu Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6675
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6675
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgccgcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtcgct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc tggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggcgaa cgtggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgatgtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttggagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcggc gaaactgaag gataaagcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaagcctg gttagctata ttagcagcct g 1371

<210> 6676
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6676
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Pro Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Leu Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Asp Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Leu Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Ala Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6677
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6677
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
cacggttcga acgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca agaagccaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagcg cgagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgcgca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgtga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6678
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6678
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ala Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6679
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6679
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgtga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6680
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6680
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6681
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6681
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
cacggttcgg gcgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgcgca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgttga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaattgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6682
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6682
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Ser Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6683
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6683
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
acaggtccgg gcgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagct cgagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcctccgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6684
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6684
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6685
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6685
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgcgca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6686
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6686
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6687
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6687
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6688
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6688
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6689
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6689
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6690
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6690
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6691
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6691
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6692
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6692
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6693
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6693
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
acaggttcgg gcgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca agaagccaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcctccgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6694
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6694
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6695
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6695
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca agaacaaaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagct cgagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960

gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6696
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6696
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Gln Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6697
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6697
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6698
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6698
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6699
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6699
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tacggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaatggaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6700
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6700
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6701
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6701
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
cacggttcgg gcgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6702
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6702
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Ser Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6703
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6703
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
acaggttcgg gcgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagct cgagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6704
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6704
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

Thr Gly Ser Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6705
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6705
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
acaggttcgg gcgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6706
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6706
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6707
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6707
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
cacggtccga acgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6708
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6708
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6709
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6709
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttccacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
cacggtccga acgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600

ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcctccgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6710
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6710
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Asn Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6711
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6711
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcag gctacctgga tacggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca agaacaaaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaatggaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6712
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6712
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Gln Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Trp Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6713
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6713
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
cacggtccga acgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tacggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaacaaaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgttgttga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctggttg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcctccgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6714
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6714
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Asn Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Gln Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Val Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6715
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6715
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca agaacaaaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6716
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6716
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Gln Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6717
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6717
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca agaagccaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6718
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6718
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6719
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6719
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
cacggttcga acgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6720
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6720
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Ser Asn Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6721
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6721
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaacaaaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagct cgagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6722
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6722
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Gln Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6723
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6723
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

cacggtccga acgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tacggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6724
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6724
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Asn Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6725
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6725
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttccacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
cacggtccgg gcgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6726
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6726
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6727
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6727
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6728
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6728
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6729
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6729
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
cacggttcgg gcgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgttga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6730
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6730
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Ser Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Val Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6731
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6731
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcag gctacctgga tacggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggaa agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6732
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6732
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6733
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6733
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca agaagccaaa 600
ccacacctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgttga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaattgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6734
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6734
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro His Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6735
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6735
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttccacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagacagagt ggcttcgcaa cctgccgacc 240
acaggtccga acgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6736
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6736
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Asn Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6737
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6737
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
acaggttcgg gcgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggacgat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca agaagccaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcacgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6738
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6738
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6739
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6739
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
cacggtccga acgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tacggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggca agaacaaaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagcg cgagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6740
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6740
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Asn Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Gln Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ala Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6741
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6741
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccattgctga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcctccgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6742
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6742
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Leu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6743
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6743
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttccacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tacggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaga cgcgcgtata gccactggaa agaacaaaaa 600
ccaatcctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagct cgagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgtga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6744
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6744
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Gln Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6745
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6745
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6746

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6746
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6747
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6747
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6748
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6748
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6749
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6749
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6750
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6750
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6751

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6751
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6752
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6752
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6753
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6753
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6754
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6754
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6755
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6755
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6756
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6756
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6757
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6757
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6758
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6758
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6759
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6759
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6760
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6760
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6761
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6761
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6762
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6762
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6763
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6763
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6764
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6764

Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6765
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6765
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaaa gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6766
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6766
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6767
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6767
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6768
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6768
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6769
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6769

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6770
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6770
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6771
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6771
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6772
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6772
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6773
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6773
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6774
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6774
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6775
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6775
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6776
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6776
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6777
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6777
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6778
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6778
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6779
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6779
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6780
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6780
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6781
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6781
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6782
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6782
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6783
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6783
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6784
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6784
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6785
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6785
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6786
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6786
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6787
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6787
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480

ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6788
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6788
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6789
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6789
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6790
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6790
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6791
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6791
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6792
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6792
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6793
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6793
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6794
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6794
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6795
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6795
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6796
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6796
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6797
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6797
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6798
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6798
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6799
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6799
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6800
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6800
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6801
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6801
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120

gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6802
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6802
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6803
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6803
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6804
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6804
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6805
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6805
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960

gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6806
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6806
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6807
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6807
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6808
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6808
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6809
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6809
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6810
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6810
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6811
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6811
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6812
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6812
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6813
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6813
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6814
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6814
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6815
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6815
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6816
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6816
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6817
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6817
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6818
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6818
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6819
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6819
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6820
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6820
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6821
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6821
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6822
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6822
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6823
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6823
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6824
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6824
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6825
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6825
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6826
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6826
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6827
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6827
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6828
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6828
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6829
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6829
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6830
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6830
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6831
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6831
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6832
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6832
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6833
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6833
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240

accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6834
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6834
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6835
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6835
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6836
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6836
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6837
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6837
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6838
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6838
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6839
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6839
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6840
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6840
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6841
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6841
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6842
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6842
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6843
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6843
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6844
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6844
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6845
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6845
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6846
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6846
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6847
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6847
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6848
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6848
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6849
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6849
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6850
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6850
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6851
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6851
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6852
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6852
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6853
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6853
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6854
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6854
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6855
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6855
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6856

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6856
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6857
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6857
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6858
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6858
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6859
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6859
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6860
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6860
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6861

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6861
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6862
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6862
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6863
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6863
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6864
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6864
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6865
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6865
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6866
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6866
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6867
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6867
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6868
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6868
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6869
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6869
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6870
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6870
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6871
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6871
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6872
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6872
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6873
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6873
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
accggtagca acgcgggtat gaccatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6874
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6874

Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Ser Asn Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6875
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6875
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgcgta gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcccgttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctgttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6876
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6876
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Arg Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Pro Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6877
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6877
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tgctgtgcct gccgcagttt 480
ttagaggcgg gctacctgga taccgaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggtgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gatctggcgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6878
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6878
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Leu Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Thr Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Val Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Leu
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6879
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6879

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagaagctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6880
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6880
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Lys Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6881
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6881
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg attcgagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6882
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6882
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Ser Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6883
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6883
atgccaaaca caaccgaaac caccaagcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6884
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6884
Met Pro Asn Thr Thr Glu Thr Thr Lys Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6885
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6885
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctgggggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6886
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6886
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Gly Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6887
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6887
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccattggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6888
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6888
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala His Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6889
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6889
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcgata gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6890
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6890
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Asp Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6891
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6891
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6892
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6892
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6893
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6893
atgcagaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6894
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6894
Met Gln Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6895
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6895
atgcataaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6896
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6896
Met His Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6897
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6897
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt atcggcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6898
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6898
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Ser Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6899
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6899
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctgcgggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6900
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6900
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Ala Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6901
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6901
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tcggttgaag gataagttgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6902
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6902
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Arg Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6903
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6903
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagcg aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6904
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6904
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Ala Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6905
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6905
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacaaggc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgtccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6906
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6906
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Lys
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 6907
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6907
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggaggaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6908
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6908
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Glu Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6909
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6909
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat cagcatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6910
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6910
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Gln His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6911
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6911
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcaggg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6912
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6912
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Gln Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6913
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6913
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgtttgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6914
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6914
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Val Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6915
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6915
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagatggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960

gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6916
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6916
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Met Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6917
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6917
atgaagaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6918
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6918
Met Lys Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6919
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6919
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcccga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6920
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6920
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Pro Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6921
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6921
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttcaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6922
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6922
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Gln Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6923
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6923
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcatggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6924
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6924
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala His Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6925
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6925
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tacttgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6926
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6926
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Thr Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6927
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6927
atgccaaaca ataccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6928
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6928
Met Pro Asn Asn Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6929
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6929
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgttgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6930
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6930
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Leu Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6931
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6931
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggacaatcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6932
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6932
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Asn Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6933
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6933
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6934
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6934
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Thr Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6935
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6935
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgtctagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6936
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6936
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Ser
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6937
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6937
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg attatagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6938
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6938
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Tyr Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6939
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6939
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaatgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6940
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6940
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Asn Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6941
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6941
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcgtga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6942
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6942
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Val Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6943
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6943
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttgcggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6944
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6944
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Ala Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6945
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6945
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tagtcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6946
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6946
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ser Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6947
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6947
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atggtagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6948
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6948
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Gly Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6949
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6949
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcactagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6950
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6950
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Thr Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6951
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6951
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atgatagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6952
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6952
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Asp Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6953
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6953
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagccgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcat aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6954
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6954
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6955
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6955
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggagtctag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6956
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6956
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Ser Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6957
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6957
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagtt aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6958
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6958
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Val Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6959
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6959
atgcggaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6960
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6960
Met Arg Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6961
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6961
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gaggttctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcat aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6962
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6962
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Val Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6963
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6963
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacataagc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6964
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6964
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Lys Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6965
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6965
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagtctggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6966

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6966
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Ser Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6967
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6967
atgccaatga caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6968
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6968
Met Pro Met Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6969
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6969
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgattc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6970
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6970
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Ile Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6971

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6971
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tctgttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6972
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6972
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Leu Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6973
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6973
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcggtcaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6974
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6974
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Gly Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6975
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6975
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttcgtgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6976
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6976
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Arg Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6977
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6977
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg ataatagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6978
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6978
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Asn Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6979
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6979
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6980
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6980
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6981
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6981
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atgagagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6982
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6982
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Glu Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6983
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6983
atgccaaaca caaccgaaac cacctctcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6984
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6984

Met Pro Asn Thr Thr Glu Thr Thr Ser Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6985
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6985
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggctttagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6986
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6986
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Phe Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6987
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6987
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgttacgct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6988
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6988
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Thr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6989
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6989

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgtct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tattttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6990
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6990
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6991
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6991
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagcc ggggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6992
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6992
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Arg Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6993
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6993
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtccgatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6994
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6994
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Pro Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6995
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6995
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6996
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6996
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Ser Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6997
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6997
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctgagggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 6998
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6998
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Glu Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 6999
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 6999
atgccattta caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7000
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7000
Met Pro Phe Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7001
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7001
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaaatt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7002
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7002
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Ile Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7003
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7003
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctaggggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7004
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7004
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Arg Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7005
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7005
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgttta gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7006
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7006
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Phe Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7007
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7007
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgaggtgg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7008
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7008
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Val Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7009
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7009
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat ttgcatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7010
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7010
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Leu His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7011
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7011
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gacgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7012
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7012
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Thr Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7013
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7013
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt agatgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7014
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7014
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Glu Ile Val Asp Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7015
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7015
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gcgaatcccg atcattaaca agcactgtgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7016
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7016
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Cys
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 7017
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7017
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat gcgcatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7018
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7018
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Ala His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7019
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7019
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggacatgcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7020
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7020
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Met Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7021
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7021
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgag 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7022
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7022
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Glu Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7023
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7023
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaatgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7024
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7024
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Asn Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7025
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7025
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaaggt aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960

gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7026
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7026
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Gly Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7027
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7027
atgatgaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7028
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7028
Met Met Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7029
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7029
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg ttatttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7030
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7030
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Tyr Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7031
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7031
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaacc gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7032
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7032
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Arg His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7033
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7033
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagactctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7034
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7034
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Thr Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7035
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7035
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct gcagcgcctg gttagctata ttagcagcct g 1371

<210> 7036
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7036
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Gln
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7037
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7037
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc gactgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7038
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7038
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Thr Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7039
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7039
atgccactta caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7040
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7040
Met Pro Leu Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7041
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7041
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aagcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7042
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7042
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Lys Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7043
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7043
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaacat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7044
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7044
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu His Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7045
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7045
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccttcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7046
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7046
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Leu Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7047
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7047
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat ccgcatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7048
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7048
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Pro His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7049
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7049
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtagtatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7050
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7050
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Ser Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7051
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7051
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgcctc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7052
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7052
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Pro Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7053
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7053
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcatttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctgttggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7054
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7054
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Ile Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Val Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7055
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7055
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagtctctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7056
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7056
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7057
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7057
atgccaaaca caaccgaaac caccgctcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgttgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7058
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7058
Met Pro Asn Thr Thr Glu Thr Thr Ala Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7059
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7059
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacttctg gttagctata ttagcagcct g 1371

<210> 7060
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7060
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Leu Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7061
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7061
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gcctgctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7062
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7062
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Leu Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7063
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7063
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgagcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7064
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7064
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Glu Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7065
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7065
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga ctgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7066
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7066
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Thr Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7067
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7067
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagcaggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7068
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7068
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Gln Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7069
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7069
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tggtttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7070
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7070
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Gly Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7071
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7071
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagccgggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7072
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7072
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Pro Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7073
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7073
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgta tgatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7074
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7074
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Met
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7075
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7075
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggttcg agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7076

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7076
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Ser Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7077
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7077
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaaggcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7078
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7078
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Lys Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7079
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7079
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg ggcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7080
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7080
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Gly Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7081

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7081
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtacgatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7082
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7082
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Thr Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7083
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7083
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagcagggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7084
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7084
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Gln Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7085
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7085
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atctgagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7086
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7086
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Leu Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7087
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7087
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atgttagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7088
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7088
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Val Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7089
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7089
atgtttaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7090
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7090
Met Phe Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7091
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7091
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agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
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ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
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agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
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caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct gaagcgcctg gttagctata ttagcagcct g 1371

<210> 7092
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7092
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Lys
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7093
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7093
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtc ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7094
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7094

Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Leu
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7095
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7095
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccggaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcac ggctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7096
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7096
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Glu Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Thr Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7097
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7097
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agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
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ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
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tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
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agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
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accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
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gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
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<210> 7098
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7098
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile His Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7099
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7099

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tgttttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7100
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7100
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Val Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7101
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7101
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tactttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7102
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7102
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Thr Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7103
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7103
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatttgc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7104
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7104
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Leu Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7105
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7105
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc gtctgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7106
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7106
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Ser Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7107
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7107
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgcttggggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7108
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7108
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Trp Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7109
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7109
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgttgtgct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7110
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7110
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Val Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7111
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7111
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgcctg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7112
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7112
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Pro Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7113
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7113
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tcagttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7114
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7114
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Gln Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7115
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7115
atgccaaaca caaccgaaac caccatgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7116
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7116
Met Pro Asn Thr Thr Glu Thr Thr Met Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7117
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7117
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480

ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tcggcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7118
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7118
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Arg Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7119
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7119
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900

agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg agcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7120
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7120
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Glu Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7121
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7121
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt actcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7122
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7122
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7123
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7123
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga atgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7124
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7124
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Asn Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7125
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7125
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg ttctttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7126
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7126
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ser Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 7127
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7127
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7128
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7128
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7129
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7129
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacattcgc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7130
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7130
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Ser Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7131
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7131
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120

agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaacgtgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7132
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7132
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Arg Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7133
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7133
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagcctctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7134
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7134
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7135
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7135
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggggg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgtct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960

gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7136
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7136
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Gly Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7137
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7137
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgactc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7138
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7138
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Thr Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7139
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7139
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctatgggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7140
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7140
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Met Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7141
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7141
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgcgatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7142
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7142
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Ala Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7143
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7143
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gaggtgtgat ttggaacagc 660
tttcatgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7144
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7144
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Arg Gly Val Ile Trp Asn Ser Phe His Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7145
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7145
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggaagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagct aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7146
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7146
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Glu Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Ala Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7147
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7147
atgccaaact cgaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7148
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7148
Met Pro Asn Ser Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7149
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7149
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaaggtctg gttagctata ttagcagcct g 1371

<210> 7150
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7150
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Gly Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7151
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7151
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg aaagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gaatcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7152
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7152
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Glu Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Asn Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7153
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7153
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg ataagagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7154
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7154
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Lys Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7155
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7155
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gaggctctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7156
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7156
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Ala Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7157
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7157
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttacttata ttagcagcct g 1371

<210> 7158
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7158
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Thr Tyr Ile Ser Ser Leu
450 455

<210> 7159
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7159
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggaaggtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7160
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7160
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Lys Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7161
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7161
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt ttgttgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7162
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7162
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Cys Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7163
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7163
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagcg cggagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7164
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7164
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Ala Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7165
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7165
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgatatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7166
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7166
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Asp Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7167
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7167
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7168
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7168
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7169
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7169
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcgaga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7170
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7170
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Glu Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7171
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7171
atggtgaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7172
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7172
Met Val Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7173
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7173
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaacct aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7174
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7174
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Pro Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7175
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7175
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaggggat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7176
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7176
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Gly Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7177
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7177
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcacacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg tgagttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7178
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7178
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Glu Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7179
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7179
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaacgt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7180
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7180
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Arg Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7181
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7181
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaac cttttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7182
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7182
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Pro
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7183
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7183
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca agggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7184
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7184
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Lys Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7185
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7185
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatattc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7186

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7186
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Ile Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7187
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7187
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggatg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7188
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7188
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Asp Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7189
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7189
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atattagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7190
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7190
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Ile Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7191

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7191
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggaagagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gttcgatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7192
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7192
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Glu Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Ser Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7193
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7193
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atgcgagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7194
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7194
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Ala Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7195
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7195
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct gagtaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7196
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7196
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Ser Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7197
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7197
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctatg ttagcagcct g 1371

<210> 7198
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7198
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Val Ser Ser Leu
450 455

<210> 7199
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7199
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ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaatctctg gttagctata ttagcagcct g 1371

<210> 7200
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7200
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7201
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7201
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taatttgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7202
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7202
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Asn Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7203
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7203
atgccaaaca caaccgaaac caccggtcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7204
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7204

Met Pro Asn Thr Thr Glu Thr Thr Gly Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7205
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7205
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaagatgat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7206
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7206
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Asp Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7207
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7207
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa agtttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7208
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7208
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Lys
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7209
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7209

atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca ttttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gaggggctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7210
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7210
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Gly Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7211
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7211
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcccgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7212
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7212
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Pro Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7213
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7213
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
agcatcacca tttttcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg caggacgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatcaaa cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcaata gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtggcgga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7214
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7214
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ser Ile Thr Ile Phe His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Asp Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Asn Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Ala Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7215
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7215
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag ccgcgaagag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7216
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7216
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7217
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7217
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcgggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag ccgcgaagag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7218
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7218
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Arg Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7219
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7219
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctta tcaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt aagggacatt 1260
agcctccgcc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7220
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7220
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Ile Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Leu Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 7221
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7221
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag ccgcgatgag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7222
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7222
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Asp Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7223
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7223
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaacagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt agcggacatt 1260
agcaaacgcc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7224
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7224
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Ala Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7225
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7225
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatcctta tcaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag ccgcgaagag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7226
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7226
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Ile Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7227
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7227
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc agaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7228
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7228
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7229
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7229
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgagagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7230
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7230
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7231
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7231
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgtcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7232
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7232
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ser Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7233
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7233
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7234
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7234
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7235
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7235
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7236
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7236
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 7237
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7237
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgatagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7238
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7238
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Ile Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7239
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7239
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7240
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7240
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7241
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7241
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7242
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7242
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7243
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7243
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7244
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7244
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7245
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7245
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgagagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7246
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7246
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7247
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7247
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7248
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7248
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7249
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7249
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7250
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7250
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7251
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7251
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgacagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7252
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7252
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Thr Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7253
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7253
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgagagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7254
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7254
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7255
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7255
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7256
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7256
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7257
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7257
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gacgatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7258
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7258
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Thr Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7259
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7259
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7260
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7260
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7261
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7261
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7262
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7262
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7263
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7263
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gacgatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgacagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7264
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7264
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Thr Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Thr Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7265
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7265
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7266
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7266
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7267
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7267
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgtcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7268
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7268
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ser Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7269
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7269
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7270
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7270
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7271
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7271
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7272
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7272
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7273
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7273
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgtcac tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7274
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7274
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ser Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7275
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7275
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7276
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7276
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7277
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7277
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7278
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7278
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7279
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7279
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgagagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7280
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7280
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7281
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7281
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgacagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7282
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7282
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Thr Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7283
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7283
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7284
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7284
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7285
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7285
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatcc attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7286
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7286
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile His Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7287
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7287
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7288
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7288
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7289
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7289
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7290
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7290
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7291
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7291
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaacaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgagagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7292
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7292
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7293
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7293
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7294
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7294
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7295
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7295
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7296

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7296
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7297
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7297
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7298
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7298
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7299
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7299
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7300
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7300
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7301

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7301
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7302
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7302
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7303
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7303
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7304
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7304
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7305
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7305
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgat cccgtgggca gaaaaagtcg cccttgaaca gacgatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7306
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7306
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Thr Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7307
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7307
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgtcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7308
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7308
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ser Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7309
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7309
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7310
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7310
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7311
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7311
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7312
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7312
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7313
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7313
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgtcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7314
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7314

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ser Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 7315
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7315
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7316
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7316
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7317
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7317
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7318
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7318
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7319
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7319

atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7320
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7320
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7321
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7321
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgatagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7322
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7322
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Ile Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7323
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7323
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7324
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7324
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7325
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7325
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7326
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7326
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7327
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7327
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
catgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgagagaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7328
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7328
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly His Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7329
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7329
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgtcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7330
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7330
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ser Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 7331
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7331
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatct atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7332
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7332
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7333
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7333
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc attatgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaacaagtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattacggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7334
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7334
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Tyr Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro

115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7335
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7335
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat cccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgttggaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7336
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7336
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Leu Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7337
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7337
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg ccgaagaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7338
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7338
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Glu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7339
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7339
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaaa 480
cgaccgggtg aagagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcggc 660
gaactgacca atgtaaaagt ggttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccatcgggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccacaag 1350

<210> 7340
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7340
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Glu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gly Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Ser Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
His Lys
450

<210> 7341
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7341
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg aagagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcggc 660
gaactgacca atgtaaaagt ggttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgccttgaag 1350

<210> 7342
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7342
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Glu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gly Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7343
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7343
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaccgggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgccttgaag 1350

<210> 7344
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7344
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7345
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7345
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcataaaagg cagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7346
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7346
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Gly Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 7347
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7347
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaaa 480
cgaccgggtg aagagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7348
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7348
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Glu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7349
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7349
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgccttgaag 1350

<210> 7350
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7350
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7351
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7351
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaagaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7352
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7352
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Arg Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7353
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7353
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcggc 660
gaactgacca atgtaaaagt ggttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccacaag 1350

<210> 7354
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7354
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gly Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
His Lys
450

<210> 7355
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7355
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcataagaaa aagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaaa 480
cgaccgggtc atgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacg 660
gaactgacca atgtaaaagt ggttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaccgggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgccttgaag 1350

<210> 7356
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7356
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Arg Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7357
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7357
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtg aagagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccacaag 1350

<210> 7358
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7358
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly Glu Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
His Lys
450

<210> 7359
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7359
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaacaggtcg ccctagaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttcaa cttcctgaaa 480
cgaccgggtc atgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaacgggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattaccgg ccccactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcccacaag 1350

<210> 7360
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7360
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gln Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Thr Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Thr Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
His Lys
450

<210> 7361
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7361
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgtgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgtcc tgctgtgcct gccgaaattt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaggccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7362
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7362
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Trp Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Val Leu Leu Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7363
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7363
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtaa gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagcgaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7364
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7364
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Lys Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7365
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7365
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtaa gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgccc tggtgtgcct gccgaaattt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagcgaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
tgtatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7366
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7366
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Cys Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7367
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7367
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtaa gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
acgatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaggccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7368
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7368
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7369
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7369
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtaa gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagcgaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7370
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7370
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7371
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7371
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtat gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcaattt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagcgaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7372
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7372
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7373
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7373
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtaa gaggatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagcgaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
tgtatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataaggccg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7374
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7374
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Cys Met Glu Ala Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7375
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7375
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagcgaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
acgatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7376
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7376
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7377
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7377
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gtgcgggtat gacgatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc agaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagcgaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7378
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7378
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Thr Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7379
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7379
atgccaaaca caagcgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtctaagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7380
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7380
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7381
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7381
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7382
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7382
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7383
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7383
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7384
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7384
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7385
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7385
atgccaaaca caagcgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg attattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggttc tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7386
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7386
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7387
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7387
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7388
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7388
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7389
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7389
atgccaaaca caagcgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
cctagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
attatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7390
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7390
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Ile Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7391
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7391
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ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7392
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7392
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7393
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7393
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7394
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7394
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7395
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7395
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ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7396
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7396
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7397
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7397
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ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggttc tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7398
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7398
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7399
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7399
atgccaaaca caagcgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg attattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7400
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7400
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7401
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7401
atgccaaaca caacccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtctaagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggttc tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7402
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7402
Met Pro Asn Thr Thr Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7403
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7403
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg actattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7404
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7404
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Thr Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7405
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7405
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg attattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7406

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7406
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7407
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7407
atgccaaaca caacccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtctaagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggttc tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
attatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7408
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7408
Met Pro Asn Thr Thr Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Ile Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7409
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7409
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
attatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7410
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7410
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Ile Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7411

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7411
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtctaagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggttc tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7412
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7412
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7413
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7413
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtctaagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7414
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7414
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7415
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7415
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7416
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7416
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7417
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7417
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7418
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7418
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7419
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7419
atgccaaaca caaccgaaac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7420
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7420
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7421
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7421
atgccaaaca caagcgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggttc tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7422
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7422
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7423
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7423
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acataaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7424
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7424

Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Ile Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7425
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7425
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgaaaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7426
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7426
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7427
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7427
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgcgagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7428
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7428
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7429
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7429

atgccaaaca caagcgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accttaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtctaagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgttccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7430
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7430
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7431
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7431
atgccaaaca caagcgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtctaagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaagtga gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7432
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7432
Met Pro Asn Thr Ser Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Leu Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7433
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7433
atgccaaaca caacccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg atcattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtag cgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gtgatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7434
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7434
Met Pro Asn Thr Thr Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Ile Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Ser Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7435
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7435
atgccaaaca caaccgagac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc accagaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga cgagaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcaagccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7436
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7436
Met Pro Asn Thr Thr Glu Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Gln Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Glu
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Lys Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7437
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7437
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacat agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gggagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7438
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7438
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7439
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7439
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7440
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7440
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7441
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7441
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaagggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacaa agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7442
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7442
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Lys Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7443
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7443
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc tgtcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7444
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7444
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Cys His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7445
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7445
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7446
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7446
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 7447
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7447
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaatggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7448

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7448
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Trp
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7449
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7449
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gggagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7450
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7450
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7451
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7451
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7452
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7452
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7453
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7453
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacat agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7454
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7454
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7455
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7455

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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7456
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7456
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7457
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7457
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180

tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagttt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gggagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7458
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7458
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7459
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7459
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7460
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7460
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7461
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7461
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7462
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7462
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7463
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7463
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacaacc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacat agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gggagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7464
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7464
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7465
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7465
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaatggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7466
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7466
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Trp
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7467
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7467
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gggagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7468
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7468
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7469
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7469
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7470
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7470
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7471
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7471
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440

ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gcaagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7472
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7472
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7473
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7473
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7474
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7474
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7475
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7475
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc ggcagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7476
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7476
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7477
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7477
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gcttgcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc ggcagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7478
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7478
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7479
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7479
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7480
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7480
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7481
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7481
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7482
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7482
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7483
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7483
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacat agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gcaagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7484
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7484
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7485
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7485
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7486
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7486
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7487
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7487
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgcgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gggagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7488
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7488
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7489
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7489
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7490
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7490

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7491
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7491
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7492
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7492
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7493
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7493
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120

aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7494
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7494
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7495
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7495
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7496
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7496
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7497
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7497
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7498
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7498
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7499
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7499
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaagggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7500
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7500
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7501
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7501
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7502
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7502
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7503
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7503
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7504
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7504
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7505
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7505
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7506
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7506
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7507
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7507
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7508
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7508
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7509
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7509
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7510
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7510
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7511
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7511
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7512
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7512
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7513
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7513
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacat agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7514
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7514
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7515
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7515
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaagggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7516
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7516
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7517
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7517
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag ctgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaagggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacat agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7518
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7518
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Ala Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7519
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7519
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacaa agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7520
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7520
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Lys Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7521
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7521
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7522
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7522
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7523

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7523
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7524
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7524
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7525
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7525
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7526
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7526
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7527
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7527
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gcaagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7528
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7528
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7529
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7529
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7530
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7530
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7531
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7531
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7532
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7532
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7533
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7533
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 7534
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7534
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His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7535
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7535
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 7536
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7536
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7537
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7537
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
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caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7538
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7538
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7539
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7539
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacaa agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7540
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7540
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Lys Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7541
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7541
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaatggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc ggcagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7542
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7542
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Trp
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7543
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7543
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7544
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7544
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7545
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7545
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7546
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7546
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7547
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7547
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaatggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7548
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7548
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Trp
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7549
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7549
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7550
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7550
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7551
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7551
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc tgtcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 7552
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7552
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Cys His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Lys Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7553
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7553
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaagggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7554
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7554
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7555
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7555
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7556
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7556
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 7557
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7557
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7558

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7558
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7559
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7559
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7560
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7560
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7561
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7561
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7562
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7562
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7563
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7563
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7564
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7564
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7565
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7565

atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gggagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7566
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7566
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gly
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7567
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7567
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180

tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7568
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7568
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7569
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7569
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaagggcttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc ggcagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7570
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7570
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7571
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7571
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc tgtcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7572
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7572
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Cys His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7573
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7573
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggacacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7574
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7574
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7575
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7575
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7576
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7576
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7577
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7577
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc tgtcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7578
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7578
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Cys His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7579
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7579
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aagcacacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gctagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7580
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7580
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ala His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7581
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7581
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttt gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaatggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc ggcagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7582
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7582
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Cys Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Trp
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Ala
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7583
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7583
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaagtcgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7584
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7584
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Val Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Ile Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Ala
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7585
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7585
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gcttgcagat 180
tttgtggcac atacccagga agcgatcttc caggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaatggcttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacag agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gcaagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7586
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7586
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Gln Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Trp
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Arg Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7587
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7587
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgca tgggtggtcc gcaagaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7588
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7588
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Met Gly Gly Pro Gln
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7589
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7589
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagcgcgcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7590
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7590
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His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Ala Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7591
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7591
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ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7592
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7592
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1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Leu Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7593
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7593
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7594
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7594
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Asn Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7595
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7595
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gcggattttc gctgtcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 7596
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7596
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Cys Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7597
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7597
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7598
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7598
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Cys Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7599
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7599
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tttgtggcac atacccagga agcgatcttc cgggagccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
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gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7600
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7600

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Glu Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7601
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7601
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7602
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7602
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Val Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7603
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7603
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga cattgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7604
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7604
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Ile Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7605
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7605
atgattgaag aactgcgcca acagctgctg gatagtccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7606
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7606
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7607
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7607
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tgttgaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7608
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7608
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Val
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7609
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7609
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcatgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7610
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7610
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Met
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7611
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7611
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtcgcgg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7612
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7612
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val Ala Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7613
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7613
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgggcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7614
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7614
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Gly Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7615
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7615
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7616
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7616
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7617
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7617
atgattgaag aactgcgcca acagctgctg gatcagccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gcccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7618
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7618
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Gln Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7619
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7619
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gctcgttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7620
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7620
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Ser Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7621
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7621
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aagttctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7622
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7622
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Val Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7623
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7623
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaggccgta ccgatggag 2379

<210> 7624
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7624
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 7625
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7625
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tccggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7626
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7626
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Pro Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7627
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7627
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtggttca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7628
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7628
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Gly Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7629
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7629
atgattgaag aactgcgcaa acagctgctg gatcttccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7630
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7630
Met Ile Glu Glu Leu Arg Lys Gln Leu Leu Asp Leu Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7631
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7631
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggagaag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7632
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7632
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Lys Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7633

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7633
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 7634
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7634
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7635
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7635
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gaacgtccgt cgtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7636
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7636
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1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Ser Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7637
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7637
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7638
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7638
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Ile Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7639
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7639
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60

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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aaaatctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7640
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7640
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Asn Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7641
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7641
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atgatggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7642
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7642
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Asp Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7643
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7643
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacaggt gccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7644
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7644
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Val Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7645
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7645
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tcaagcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7646
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7646
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Lys Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7647
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7647
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccctcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7648
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7648
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Pro Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7649
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7649
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
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actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 7650
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7650
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp His Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7651
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7651
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7652
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7652
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Val Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7653
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7653
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ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7654
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7654
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7655
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7655
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gcggattttg tggaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7656
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7656
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Val Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7657
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7657
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggccggca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7658
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7658
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Arg
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7659
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7659
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7660
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7660
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Ala Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7661
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7661
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gcggattttc tggaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7662
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7662
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Leu Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7663
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7663
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
ctgattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7664
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7664
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Leu Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7665
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7665
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cgtcatttag tcgcatctca gcgtccgtca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7666
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7666
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Pro Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 7667
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7667
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagcaagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7668

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7668
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Lys Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7669
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7669
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggagg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7670
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7670
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7671
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7671
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcgtgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7672
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7672
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Val
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7673
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7673
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gcggattttc gcgaacagtg tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7674
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7674
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Cys Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7675
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7675

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gcggattttc gcgctcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7676
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7676
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7677
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7677
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180

tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcgctgg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7678
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7678
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Ala Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7679
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7679
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaagtgg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7680
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7680
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Val Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7681
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7681
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctag gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7682
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7682
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Arg Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7683
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7683
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa gcggaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagt gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7684
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7684
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Ala Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7685
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7685
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aaactctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7686
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7686
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7687
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7687
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcctgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7688
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7688
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Leu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7689
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7689
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tctgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7690
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7690
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Cys Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7691
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7691
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagtactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440

ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7692
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7692
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Ala Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
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660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
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Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7693
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

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<210> 7694
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7694
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His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Asn Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
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His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
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Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
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Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
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485 490 495
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660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7695
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
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<210> 7696
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7696
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His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
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Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
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Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His His Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
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Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
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Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
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Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
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305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
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Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
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Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
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Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
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Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
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690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
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770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7697
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

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<210> 7698
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<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7698
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His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Gly Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7699
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7699
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagctttcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160

gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7700
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7700
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Phe Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7701
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7701
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagac tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7702
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7702
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Thr Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7703
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7703
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggatttttc gcgaacagtt gccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7704
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7704
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7705
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7705
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccgg gtgtttggga gtatgtgcgc attcatgtag aactgctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7706
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7706
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Leu Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7707
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7707
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aagatctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7708
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7708
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Asp Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7709
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7709
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtttgtca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
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caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7710
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7710

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Leu Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7711
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7711
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
actattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7712
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7712
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Thr Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7713
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7713
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120

gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcactca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7714
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7714
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7715
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7715
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggagccg 300

ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7716
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7716
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Pro Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7717
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7717
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggagcag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7718
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7718
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Gln Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7719
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7719
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gctgtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7720
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7720
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Cys Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7721
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7721
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaggttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaagtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7722
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7722
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Arg Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7723
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7723
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7724
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7724
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7725
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7725
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7726
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7726
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7727
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7727
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gcggattttc gcgaacagga tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7728
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7728
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Asp Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7729
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7729
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttaaa gcgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7730
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7730
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Lys Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7731
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7731
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
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cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7732
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7732
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Ala Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7733
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7733
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc cctcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggccgtg gcgtttttgt gcaaccagcc 1980
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7734
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7734
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Pro Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7735
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7735
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gcggattttc gcgaacagcc tgcggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7736
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7736
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Ala
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7737
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7737
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg taggaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7738
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7738
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7739
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7739
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag attctggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7740
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7740
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ser Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7741
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7741
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagcaatcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7742
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7742
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Asn Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7743

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7743
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc agtcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7744
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7744
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Ser Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7745
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7745
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
tcgtatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7746
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7746
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Ser Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7747
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7747
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaggac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7748
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7748
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7749
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7749
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta ttcggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7750
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7750
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Ser Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7751
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7751
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgat tccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7752
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7752
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Ile Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7753
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7753
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaggaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtctg aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7754
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7754
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7755
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7755
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tcatgcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7756
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7756
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Met Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7757
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7757
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacggg 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7758
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7758
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Gly Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7759
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7759
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcagtcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggaa 2379

<210> 7760
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7760
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Ser Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7761
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7761
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gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggctttgg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7762
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7762
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Phe Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7763
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7763
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
gcggattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc attcatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaaggacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaaccagg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccaggagatt 1440
ggtcaatatg aaggtcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgct tcggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 7764
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7764
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Ala Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gly
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Gln Glu Ile
465 470 475 480
Gly Gln Tyr Glu Gly His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg Phe Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 7765
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7765
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atcccagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7766
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7766
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7767
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7767
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atcccagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7768
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7768
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7769
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7769
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagagactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7770
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7770
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Arg Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7771
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7771
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc ataggagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgagagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7772
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7772
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Arg Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7773
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7773
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7774
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7774
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7775
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7775
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaactggatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7776
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7776
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Leu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7777
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7777
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc ataggagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgagagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7778
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7778
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Arg Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7779
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7779
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaactggatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7780
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7780
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Leu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7781
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7781
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc ataagagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgagagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7782

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7782
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Lys Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7783
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7783
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7784
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7784
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7785
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7785
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7786
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7786
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7787

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7787
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaactggatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc ataagagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7788
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7788
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Leu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Lys Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7789
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7789
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7790
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7790
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7791
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7791
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaactggatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7792
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7792
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Leu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7793
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7793
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7794
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7794
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7795
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7795
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aagcgcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagttccc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7796
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7796
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Ala Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7797
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7797
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gcttaccgaa 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atcccagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7798
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7798
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7799
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7799
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaactggatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7800
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7800

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Leu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 7801
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7801
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaacgattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7802
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7802
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Thr Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7803
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7803
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atcccagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagagactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7804
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7804
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Arg Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7805
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7805

atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc ataagagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7806
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7806
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Lys Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7807
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7807
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7808
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7808
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7809
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7809
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgagagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7810
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7810
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Arg
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7811
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7811
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aagcgcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atcccagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagagactgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7812
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7812
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Ala Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Arg Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7813
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7813
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aagcgcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7814
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7814
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Ala Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7815
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7815
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaactggatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatcttgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7816
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7816
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Leu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Leu Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 7817
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7817
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc ctttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7818
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7818
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7819
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7819
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggac gaactggatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7820
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7820
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Leu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7821
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7821
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggaa atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atcccagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7822
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7822
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Glu Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7823
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7823
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga actggcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7824
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7824
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Leu Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7825
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7825
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gagaaggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccatgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcccacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacggc tgagagcgcg ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7826
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7826
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser His
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Pro Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7827
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7827
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gagagggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcccacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7828
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7828
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Arg Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Pro Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7829
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7829
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgcg ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7830
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7830
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7831
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7831
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgcg ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7832
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7832
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 7833
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7833
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagtat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gagggtgtcg cccttaggca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccactgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7834
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7834
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gly Val Ala Leu Arg Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7835
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7835
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gagagggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccactgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcccacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7836
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7836
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Arg Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Pro Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7837
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7837
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7838
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7838
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7839
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7839
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gagggtgtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7840
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7840
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gly Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7841
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7841
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacggc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7842
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7842
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7843
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7843
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7844
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7844
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7845
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7845
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7846
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7846
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7847
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7847
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccactgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7848
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7848
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7849
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7849
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccatgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7850
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7850
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser His
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7851
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7851
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gagaaggtcg cccttgaaca ggggatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7852
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7852
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7853
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7853
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gagagggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7854
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7854
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Arg Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7855
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7855
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaca cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7856
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7856
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
His Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7857
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7857
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gagaaggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccactgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcccacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7858
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7858
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Pro Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7859
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7859
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gagaaggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaattcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgcg ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7860
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7860
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7861
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7861
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gagagggtcg cccttaggca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacggc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7862
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7862
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Arg Val Ala Leu Arg Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7863
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7863
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7864
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7864
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7865
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7865
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gagaaggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7866
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7866
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7867
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7867
atgcaccatc atcatgaagt cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gagggtgtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcccacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgcg ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7868
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7868
Met His His His His Glu Val Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Gly Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Pro Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7869
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7869
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7870
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7870
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7871
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7871
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaattcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7872
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7872
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7873
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7873
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7874
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7874
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7875
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7875
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gagaaggtcg cccttaggca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tccttcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7876
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7876
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Arg Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Leu Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7877
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7877
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccatgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccactgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7878
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7878
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser His
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7879
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7879
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300
gctctgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gagggtgtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccactgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaactgc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7880
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7880
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Gly Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Leu Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7881
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7881
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaattcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tctcacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7882
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7882
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ser Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ser Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7883
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7883
atgcaccatc atcatgaagg cgtgagcgat cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcaata gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcgtaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7884
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7884
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Asn Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu Arg Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7885
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7885
atgcaccatc atcatgaagg cgtgagcggt cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaga gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcacc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcataag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgat tccgtgggca gagaaggtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcg 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacggc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7886
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7886
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7887
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7887
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcatg 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggggaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgcaa tgcctataag 1350

<210> 7888
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7888
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Met Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7889
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7889
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgcaa tgccaagaag 1350

<210> 7890
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7890
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Asn Ala
435 440 445
Lys Lys
450

<210> 7891
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7891
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa tgccctcaag 1350

<210> 7892

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7892
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7893
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7893
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgccaaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7894
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7894
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7895
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7895
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgccaaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa tgccctcaag 1350

<210> 7896
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7896
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7897

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7897
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacg 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccacccggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgctt agccctcaag 1350

<210> 7898
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7898
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Leu Ala
435 440 445
Leu Lys
450

<210> 7899
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7899
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgagagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgcaa tgccaggaag 1350

<210> 7900
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7900
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Arg Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Asn Ala
435 440 445
Arg Lys
450

<210> 7901
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7901
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccacccggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggggaaat tgcccaagtc 1200
ctgagagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7902
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7902
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Arg Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7903
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7903
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgccaaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgctt agccaggaag 1350

<210> 7904
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7904
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Leu Ala
435 440 445
Arg Lys
450

<210> 7905
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7905
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgctt agcctataag 1350

<210> 7906
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7906
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Leu Ala
435 440 445
Tyr Lys
450

<210> 7907
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7907
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgcaa tgccctcaag 1350

<210> 7908
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7908
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7909
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7909
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccacccggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggggaaat tgccaaagtc 1200
ctgaaagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa tgccctcaag 1350

<210> 7910
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7910

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Leu Lys
450

<210> 7911
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7911
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacg 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgcaa tgccctcaag 1350

<210> 7912
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7912
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7913
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7913
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacg 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgcaa tgccaagaag 1350

<210> 7914
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7914
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Asn Ala
435 440 445
Lys Lys
450

<210> 7915
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7915

atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
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ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgctt agccctcaag 1350

<210> 7916
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7916
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Leu Ala
435 440 445
Leu Lys
450

<210> 7917
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7917
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacg 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgctt agccaggaag 1350

<210> 7918
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7918
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Leu Ala
435 440 445
Arg Lys
450

<210> 7919
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7919
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggggaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgctt agccctcaag 1350

<210> 7920
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7920
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Leu Ala
435 440 445
Leu Lys
450

<210> 7921
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7921
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggggaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgcaa tgccaggaag 1350

<210> 7922
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7922
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445
Arg Lys
450

<210> 7923
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7923
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagccgccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggggaaat tgcccaagtc 1200
ctgaaagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgctt agccctcaag 1350

<210> 7924
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7924
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Arg Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Leu Ala
435 440 445
Leu Lys
450

<210> 7925
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7925
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaagcgctt agcctataag 1350

<210> 7926
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7926
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Leu Ala
435 440 445

Tyr Lys
450

<210> 7927
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7927
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggggaaat tgcccaagtc 1200
ctgagagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgcaa tgccctcaag 1350

<210> 7928
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7928
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Arg Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Asn Ala
435 440 445
Leu Lys
450

<210> 7929
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7929
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccacccggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgctt agcctataag 1350

<210> 7930
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7930
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Leu Ala
435 440 445
Tyr Lys
450

<210> 7931
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7931
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagccgccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgccaaagtc 1200
ctgagagatg tgattggcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7932
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7932
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Arg Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Arg Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7933
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7933
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacg 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgctt agccctcaag 1350

<210> 7934
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7934
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Leu Ala
435 440 445
Leu Lys
450

<210> 7935
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7935
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgctt agcctataag 1350

<210> 7936
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7936
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Leu Ala
435 440 445
Tyr Lys
450

<210> 7937
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7937
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcccg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccacccggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaagcgctt agccctcaag 1350

<210> 7938
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7938
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Pro Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Leu Ala
435 440 445
Leu Lys
450

<210> 7939
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7939
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaggcgcaa tgccaggaag 1350

<210> 7940
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7940
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Arg Arg Asn Ala
435 440 445
Arg Lys
450

<210> 7941
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7941
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgccaaagtc 1200
ctgaaagatg tgattagcgg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7942
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7942
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 7943
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7943
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtgggagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgcccc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtag cccttgaaca gggcatcccg 420
gctgttaaag ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgccaa 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 7944
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7944
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Lys Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Gln Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 7945
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7945
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgtcgg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaatggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7946
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7946
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7947
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7947
atgccaaaca caagccccac caccgttcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120

gcgatcacca ttctgcacac caacttcaac gccccggaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgtcgg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcagc gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaaatt ctgcatgtgg gcattacgct ggagaatggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7948
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7948
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Glu Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Ile Leu His Val Gly Ile Thr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7949
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7949
atgccaaaca caagccccac caccggtcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7950
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7950
Met Pro Asn Thr Ser Pro Thr Thr Gly Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7951
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7951
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgtcgg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960

gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgttacgct ggagaatggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7952
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7952
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Thr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7953
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7953
atgccaaaca caagccccac caccgttcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccggaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgtcgg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcagc gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttacct ggagaatggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg tatattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7954
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7954
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Glu Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7955
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7955
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7956
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7956
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7957
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7957
atgccaaaca caagccccac caccgttcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttcgc gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7958
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7958
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Ser Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7959
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7959
atgccaaaca caagccccac caccgttcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgcttc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaga atgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg tatattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7960
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7960
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Leu Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Asn Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7961
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7961
atgccaaaca caagccccac caccggtcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggatg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgttacgct ggagaatggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7962
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7962
Met Pro Asn Thr Ser Pro Thr Thr Gly Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Asp Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Thr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7963
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7963
atgccaaaca caagccccac caccggtcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7964
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7964
Met Pro Asn Thr Ser Pro Thr Thr Gly Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7965
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7965
atgccaaaca caagccccac caccgttcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggatg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgttacgct ggagaatggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7966
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7966
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Asp Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Thr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7967
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7967
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg tatattgaag gataagttgg atcgaagcct tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7968
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7968
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300

Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7969
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7969
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccggatg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaga atgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7970
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7970
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Asp Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Asn Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7971
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7971
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgtcgg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcagc gggaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgttacgct ggagcaaggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7972
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7972
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Thr Leu Glu Gln Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7973
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7973
atgccaaaca caagccccac caccgttcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccggaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga atgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7974
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7974
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Glu Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Asn Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7975
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7975
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttgga atgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttacct ggagaatggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7976
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7976
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Asn Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7977
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7977
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg aaagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttgccgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7978
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7978
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Glu Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Ala Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7979
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7979
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7980
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7980
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7981
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7981
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg aaagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7982
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7982
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Glu Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7983
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7983
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg aaagaagcat tagtcatggt 1320
ggctctagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7984
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7984
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Glu Arg Ser Ile Ser His Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7985
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7985
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat ccgcatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7986
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7986
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Pro His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7987
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7987
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccag gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagtcactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7988
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7988
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7989
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7989
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7990
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7990
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7991
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7991
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7992
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7992
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7993
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7993
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgttat ttggaacagc 660
tttgccgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atataagcat tgcccctggt 1320
ggctttagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7994
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7994
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Ala Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Ile Ser Ile Ala Pro Gly Gly Phe Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7995
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7995
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg atagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttgccgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcactg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagtcactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atgaaagcat tgcccctggt 1320
ggctttagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7996
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7996
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Ala Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Glu Ser Ile Ala Pro Gly Gly Phe Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7997
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7997
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg aaagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 7998
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7998
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Glu Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 7999
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 7999
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg atagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtag cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataaggcag atatcagcat taggcctggt 1320
ggctttagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8000
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8000
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Ala Asp Ile Ser Ile Arg Pro Gly Gly Phe Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8001
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8001
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8002

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8002
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8003
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8003
atgaaaatga caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtag cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataaggcag atgaaagcat tgcccctggt 1320
ggctttagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8004
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8004
Met Lys Met Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Ala Asp Glu Ser Ile Ala Pro Gly Gly Phe Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8005
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8005
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8006
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8006
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8007

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8007
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttgccgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8008
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8008
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Ala Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8009
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8009
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg atagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttgccgagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccaaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtag cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttactgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgacttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8010
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8010
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Ala Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8011
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8011
atgaaaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8012
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8012
Met Lys Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8013
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8013
atgccgaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgctccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtag cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgcccatggt 1320
ggctctagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8014
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8014
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala His Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8015
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8015
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgagatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8016
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8016
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8017
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8017
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagagttgg gccttctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8018
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8018
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Leu Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8019
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8019
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgaaattt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagctcga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8020
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8020

Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8021
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8021
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8022
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8022
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8023
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8023
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8024
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8024
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Thr Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8025
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8025

atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgaaattt 480
ttagaggcag gccttctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8026
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8026
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Leu Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Thr Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8027
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8027
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8028
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8028
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8029
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8029
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgtgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtcccatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8030
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8030
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Val Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Thr Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Pro Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8031
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8031
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagaggcag gccttctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8032
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8032
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Leu Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8033
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8033
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcgaaa gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8034
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8034
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Glu Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8035
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8035
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8036
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8036
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8037
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8037
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagaggcag gccttctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagcc gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gcattatagg gcgagctcga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8038
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8038
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Leu Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Arg Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8039
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8039
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagcc gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8040
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8040
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Arg Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8041
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8041
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagcc gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8042
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8042
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Arg Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8043
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8043
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480

ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8044
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8044
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8045
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8045
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgattc cgctgccgaa gtggtatagg gcgagctcga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900

agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8046
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8046
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Ile Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8047
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8047
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8048
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8048
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8049
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8049
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgaaattt 480
ttagagttgg gctacctgga tccggacgat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagcc gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtcccatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8050
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8050
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Arg Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Pro Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8051
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8051
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8052
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8052
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 8053
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8053
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8054
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8054
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Thr Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8055
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8055
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagctcga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8056
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8056
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8057
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8057
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120

gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8058
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8058
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala

180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Thr Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8059
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8059
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8060
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8060
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8061
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8061
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gccttctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960

gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8062
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8062
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Leu Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser

290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8063
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8063
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtcccatcgt taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8064
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8064
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Pro Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8065
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8065
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8066
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8066
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Thr Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8067
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8067
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagcc gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8068
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8068
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Arg Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8069
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8069
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcgaaa gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8070
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8070
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Glu Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8071
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8071
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgat 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8072
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8072
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8073
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8073
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtcccatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8074
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8074
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Pro Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8075
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8075
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcaattt 480
ttagagttgg gccttctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagcacga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8076
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8076
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Leu Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Thr Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8077
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8077
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8078
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8078
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300

Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8079
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8079
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgcaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gtggtatagg gcgagctcga gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcgt taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8080
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8080
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys Trp Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8081
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8081
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8082
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8082
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8083
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8083
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
tcatttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtcccatcgt taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8084
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8084
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Pro Ile Val Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8085
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8085
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggaa agaagcaaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccatttgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8086
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8086
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Ile Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8087
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8087
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8088
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8088
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8089
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8089
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaagtaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtcccatcgt taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8090
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8090
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Val Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Pro Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8091
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8091
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt cagctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8092
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8092
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Gln Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8093
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8093
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaact gtgcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8094
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8094
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Cys Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8095
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8095
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaatacc gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8096
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8096
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8097
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8097
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttacagag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8098
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8098
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Gln Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8099
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8099
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttattgag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8100
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8100
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Leu Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8101
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8101
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
tttgttatcc atctcgttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8102
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8102
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8103
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8103
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttatgtag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8104
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8104
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Cys Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8105
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8105
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttaactag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8106
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8106
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Thr Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8107
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8107
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccaagatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8108
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8108
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Lys Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8109
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8109
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccgacgctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccacctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8110
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8110
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Thr Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8111
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8111
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttaatga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8112

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8112
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Asn Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8113
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8113
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactagg gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8114
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8114
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Arg Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8115
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8115
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac gaacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtggtct gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8116
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8116
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ser Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8117

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8117
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccaatatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8118
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8118
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Asn Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8119
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8119
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tcggcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8120
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8120
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Arg Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8121
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8121
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcacggt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8122
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8122
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Thr Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8123
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8123
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacttt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8124
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8124
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Phe Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8125
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8125
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaac agatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8126
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8126
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Gln Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8127
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8127
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt cctctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8128
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8128
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Pro Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8129
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8129
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
tgtgtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8130
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8130

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Cys Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 8131
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8131
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gtcggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8132
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8132
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Ser Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8133
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8133
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaaa ctatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8134
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8134
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Thr Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8135
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8135

atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaatacg gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8136
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8136
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Gly
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8137
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8137
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tcatcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcatacaag 1350

<210> 8138
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8138
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile His Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8139
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8139
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaacatg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8140
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8140
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys His Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8141
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8141
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccgggtctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8142
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8142
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Gly Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8143
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8143
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa ggcggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8144
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8144
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Ala Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8145
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8145
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccggtatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8146
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8146
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Gly Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 8147
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8147
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacagg 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8148
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8148
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Arg Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8149
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8149
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gtcgggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8150
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8150
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Ser Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8151
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8151
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcga gttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8152
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8152
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Glu Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8153
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8153
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtactgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8154
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8154
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Thr Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8155
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8155
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gctggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8156
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8156
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Leu Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8157
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8157
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
caggttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8158
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8158
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Gln Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8159
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8159
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagattaag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8160
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8160
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Ile Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8161
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8161
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttacgt atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8162
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8162
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Thr Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 8163
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8163
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctggaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8164
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8164
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8165
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8165
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8166
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8166
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8167
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8167
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
ctgctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8168
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8168
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Leu Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8169
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8169
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaactc taactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8170
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8170
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8171
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8171
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc cggttttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccacctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8172
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8172
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Gly Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8173
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8173
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgctttcgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8174
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8174
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Ser Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8175
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8175
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttctcggt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8176
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8176
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Ser Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8177
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8177
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt actctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8178
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8178
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8179
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8179
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaact ggcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8180
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8180
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Leu Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8181
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8181
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacctg 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8182
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8182
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Leu Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8183
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8183
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt acgctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8184
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8184
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8185
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8185
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt atgctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8186
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8186
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Met Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8187
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8187
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccgagtctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8188
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8188
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Ser Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8189
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8189
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat taagcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8190
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8190
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Lys Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8191
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8191
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgagtc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8192
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8192
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Ser His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8193
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8193
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaactt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8194
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8194
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Leu Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8195
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8195
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8196
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8196
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8197
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8197
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcggg ggaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8198
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8198
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Gly Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8199
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8199
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccacctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatc 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacttg 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8200
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8200
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Leu Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8201
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8201
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccacctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga tgaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8202
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8202
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Asp Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8203
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8203
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgcgatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8204
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8204
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ala Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8205
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8205
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgc gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8206
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8206
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ala Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8207
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8207
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
ggtgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8208
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8208
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Gly Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8209
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8209
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttaa taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacttgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8210
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8210
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Asn Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8211
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8211
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa ggctgacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cgcgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8212
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8212
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Ala Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Ala Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8213
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8213
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
agtctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8214
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8214
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Ser Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8215
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8215
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa ggttgacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8216
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8216
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Val Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8217
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8217
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaatact tgaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8218
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8218
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Leu
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8219
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8219
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct accaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaatg tcgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8220
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8220
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Cys Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8221
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8221
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atttggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8222

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8222
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Leu Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8223
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8223
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttggtga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8224
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8224
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Gly Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8225
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8225
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcggt ggaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8226
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8226
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Val Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8227

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8227
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgcgat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8228
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8228
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Ala Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8229
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8229
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccacattt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8230
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8230
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro His Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8231
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8231
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaaaaacgtg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8232
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8232
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Arg Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8233
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8233
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacggggt gctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8234
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8234
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Val Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8235
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8235
atgacgcatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8236
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8236
Met Thr His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8237
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8237
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagactcttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8238
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8238
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Thr
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8239
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8239
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctacacaag 300
gcactgaaga tgagcgctcc caactttagc aagaatcttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8240
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8240

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Asn
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 8241
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8241
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttcac tttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8242
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8242
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Thr Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8243
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8243
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgtgagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8244
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8244
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8245
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8245

atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaatacg cgaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8246
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8246
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ala
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8247
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8247
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caaccttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8248
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8248
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Leu Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8249
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8249
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
acgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8250
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8250
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Thr Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8251
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8251
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaaagtg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8252
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8252
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Ser Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8253
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8253
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaactc gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8254
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8254
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8255
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8255
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggcgctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8256
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8256
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Ala Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 8257
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8257
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacaa gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8258
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8258
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Lys Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8259
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8259
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gattgacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8260
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8260
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Ile Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8261
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8261
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttctgt atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8262
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8262
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Leu Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8263
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8263
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc acggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgactgg 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8264
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8264
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu

225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His His Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Trp Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8265
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8265
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc cacgtttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8266
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8266
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Thr Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8267
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8267
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttcgtga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8268
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8268
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Arg Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8269
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8269
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8270
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8270
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8271
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8271
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag ttctgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgtccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8272
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8272
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Ser
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Val Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 8273
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8273
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaattttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgcgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8274
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8274
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Ala Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8275
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8275
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagcagcttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8276
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8276
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Gln
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8277
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8277
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
catcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8278
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8278
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys His Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu

180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8279
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8279
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaattgg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8280
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8280
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Leu Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240

Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8281
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8281
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtct ctcttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8282
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8282
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ser Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8283
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8283
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttctg tttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8284
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8284
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Cys Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8285
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8285
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt gtgctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8286
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8286
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Val Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8287
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8287
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgagcc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tactcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8288
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8288
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Ser His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Thr Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8289
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8289
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
actcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8290
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8290
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Thr Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8291
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8291
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggct gctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8292
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8292
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Leu Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8293
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8293
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcagtat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8294
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8294
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190

Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Ser Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8295
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8295
atgcaccatt ttcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8296
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8296
Met His His Phe His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8297
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8297
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
tctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8298
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8298
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ser Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8299
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8299
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aaggtgcttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8300
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8300
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Val
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8301
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8301
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgatatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gtgcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8302
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8302
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Asp Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Cys Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8303
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8303
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaatacg ttaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8304
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8304
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Val
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8305
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8305
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccactgtt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8306
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8306
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Leu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8307
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8307
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgag gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcac tttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cggaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8308
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8308
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Arg Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Thr Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Arg Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8309
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8309
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8310
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8310
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8311
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8311
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaatacc agaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8312
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8312
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Gln
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8313
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8313
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaaag tcgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactaata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8314
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8314
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Ser Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8315
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8315
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgcgatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
cctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8316
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8316
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ala Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Pro Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8317
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8317
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8318
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8318
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8319
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8319
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggg ggatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8320
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8320
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Gly Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8321
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8321
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagaggcttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8322
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8322
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Arg
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8323
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8323
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatgt atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8324
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8324
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Met Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8325
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8325
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactatagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8326
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8326
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Tyr Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8327
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8327
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720

gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcac tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8328
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8328
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Thr Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8329
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8329
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acagaggaag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8330
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8330
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Arg Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8331
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8331
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttgcgt atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8332

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8332
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ala Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8333
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8333
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtcag 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8334
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8334
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gln Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8335
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8335
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgggatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8336
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8336
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Gly Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8337

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8337
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaatact ttaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaacctgaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccggat gaagaagatc cgttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gatgaccgaa 720
gatatcgacg acaaagaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatcctgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8338
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8338
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Phe
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Asp Glu Glu
180 185 190
Asp Pro Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Met Thr Glu
225 230 235 240
Asp Ile Asp Asp Lys Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8339
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8339
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggctttctaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8340
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8340
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8341
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8341
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8342
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8342
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8343
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8343
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc tgtgccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8344
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8344
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Val Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8345
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8345
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagcctgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8346
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8346
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Pro Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8347
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8347
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
gattttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8348
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8348
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Asp Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8349
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8349
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ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagcgatta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8350
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8350

Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Asp Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8351
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8351
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ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgt gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8352
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8352
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Val Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8353
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8353
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ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
gagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
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accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
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ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8354
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8354
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Glu Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8355
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8355

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gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gatgatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8356
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8356
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Met Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8357
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8357
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gcttatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8358
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8358
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Leu Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8359
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8359
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagtct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8360
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8360
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8361
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8361
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gagatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8362
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8362
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Glu Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8363
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8363
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaatcgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8364
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8364
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Asn Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8365
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8365
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcac gaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8366
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8366
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Thr Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8367
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8367
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gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
agctttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtga gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgcagttt 480
ttagagcttg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca ggaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgac 900
agcaaacaaa gctttctgtg gcgggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
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caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgaaatcgt aaacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8368
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8368
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Ser Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Glu Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Gln Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser
290 295 300
Phe Leu Trp Arg Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Val Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8369
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8369
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgcacagat tccggaaggc ccacccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagcccgcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagcggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtctt ccgattttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8370
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8370
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Ala Gln Ile Pro
35 40 45
Glu Gly Pro Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Pro Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Arg Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8371
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8371
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgcacagcc tccggaaggc ccacccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagcccgcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gctgcggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgttt ccagttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8372
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8372
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Pro Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Pro Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Cys Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gln Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8373
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8373

atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
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aaagattttc gcgcacagcc tccggaaggc ccacccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagcggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgttt cggattttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8374
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8374
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Pro Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile

465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8375
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8375
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc taccccgaag atattggttg gctggcagat 180

tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagcccgcg tttaaaagac 420
gagaacacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagcggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8376
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8376
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Pro Arg Leu Lys Asp Glu Asn Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8377
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8377
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaagagac 420
gagaacacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8378
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8378
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Asn Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8379
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8379
atgattgaag aactgcgcca acagctgctg gatgtcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgcacagat tccggaaggc taccccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagaacacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gctgcggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtctt ccagttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8380
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8380
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Val Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Ala Gln Ile Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Asn Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Cys Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gln Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8381
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8381
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgcacagct tccggaaggc taccccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8382
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8382
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Val Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Ala Gln Leu Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8383
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8383
atgattgaag aactgcgcca acagctgctg gatgtcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 8384
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8384
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His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Asn Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gln Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8385
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8385
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 8386
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8386
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8387
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8387
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8388
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8388
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Ala
35 40 45
Glu Gly Pro Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gln Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8389
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8389
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaagagac 420
gagaacacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440

ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
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<210> 8390
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8390
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Ala Gln Ile Ala
35 40 45
Glu Gly Ser Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Asn Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8391
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8391
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaagagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgttt ccagttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8392
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8392
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Ile Pro
35 40 45
Glu Gly Ser Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gln Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8393
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8393
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaggccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga gctattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8394
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8394
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro Ser Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8395
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8395
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagcctg 1620
ctgtttgggc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8396
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8396
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8397
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8397
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatacct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcggaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagccg 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160

gaacgtccgc attattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8398
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8398
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8399
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8399
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatacct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcgggccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
gttattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgg gctattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8400
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8400
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Gly Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8401
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8401
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcggaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8402
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8402
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8403
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8403
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatggct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaggccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gataggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8404
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8404
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Trp Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8405
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8405
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8406
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8406
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8407
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8407
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcggaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8408
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8408

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8409
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8409
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatacct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcggaccgta 600
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cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
gttattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8410
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8410
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8411
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8411
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120

aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatacct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8412
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8412
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8413
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8413
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcgggccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagccg 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8414
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8414
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8415
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8415
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatacct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
gttattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8416
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8416
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8417
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8417
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatacct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcgggccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
gttattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8418
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8418
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8419
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8419
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8420
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8420
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8421
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8421
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagccg 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8422
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8422
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8423
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8423
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8424
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8424
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8425
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8425
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatacct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctgggtcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8426
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8426
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8427
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8427
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gataggcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc ggtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8428
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8428
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Arg Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8429
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8429
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8430
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8430
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8431
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8431
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcgggccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagccg 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gttattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8432
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8432
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Pro
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8433
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8433
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8434
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8434
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Gly Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Lys Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8435
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8435
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaggccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagtctg 1620
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gttattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc attattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8436
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8436
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Val Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8437
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8437
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cgtcatttag tcgaatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
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gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8438
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8438
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Glu Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8439
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8439
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atataggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg cgttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaaa 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaagatggt 1080
acgattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggcgt 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaggccgta ccgatggag 2379

<210> 8440
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8440
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Thr Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 8441

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8441
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc acttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaagatggt 1080
aggattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggcct 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8442
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8442
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8443
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8443
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgaatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggagaaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg cgttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaaa 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaagatggt 1080
aggattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggcgt 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg acatggaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaggccgta ccgatggag 2379

<210> 8444
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8444
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Glu Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Lys Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Met Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 8445
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8445
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cgtcatttag tcgaatctca gcgtccgtca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacaactggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc acttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaaa 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggcgt 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8446
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8446
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Glu Ser Gln Arg Pro Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8447
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8447
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacaactggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc acttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacggt 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggcgt 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8448
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8448
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Gly Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480

Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8449
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8449
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacaactggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8450
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8450
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8451
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8451
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atgacggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacaactggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc acttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaaa 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaagatggt 1080
aggattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaggccgta ccgatggag 2379

<210> 8452
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8452
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Asp Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 8453
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8453
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atgacggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacaactggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8454
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8454
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Asp Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8455
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8455
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atgacggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8456
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8456
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Asp Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8457
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8457
atgattgaag aactgcgcca acggctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgaatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atgacggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc acttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaaa 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta ttccgatggt 1080
aggattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattgggta 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaggccgta ccgatggag 2379

<210> 8458
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8458
Met Ile Glu Glu Leu Arg Gln Arg Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Glu Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Asp Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Ser Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Val Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 8459
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8459
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtccgtca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atataggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacaactggc ggtggaggaa 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc acttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaaa 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaagatggt 1080
acgattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggca atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaggccgta ccgatggag 2379

<210> 8460
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8460
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Pro Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Thr Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 8461
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8461
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8462
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8462
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8463
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8463
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atgacggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc acttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaagc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggcgt 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaggccgta ccgatggag 2379

<210> 8464
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8464
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Asp Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 8465
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8465
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacggg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680

ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgggaagaaa tcaggcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8466
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8466
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8467
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8467
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt ggcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcatgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacggg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacaa agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgggaagaaa tcatgcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8468
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8468
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Leu Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Met
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Lys Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Met Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8469
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8469
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcaac cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacggg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgcc 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8470
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8470
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Asn Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8471
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8471
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttcgg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgcc 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca agactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgggaagaaa tcaggcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8472
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8472
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Phe Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8473
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8473
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aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatacc 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8474
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8474
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Thr Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 8475
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8475
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcactca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tcaggcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8476

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8476
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8477
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8477
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcaac cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgcc 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8478
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8478
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Asn Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8479
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8479
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaagattttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacat tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgcc 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgagatt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
ctgattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa caggaagaaa tcaggcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccgc actattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8480
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8480
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Asp Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Ile Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Ile
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Leu Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Gln Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro His Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8481
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8481
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8482
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8482
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8483
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8483
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtaa gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8484
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8484
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8485
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8485
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8486
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8486
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8487
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8487
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8488
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8488
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8489
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8489
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8490
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8490
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8491
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8491
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8492
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8492
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8493
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8493
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8494
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8494
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn

35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8495
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8495
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8496
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8496
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8497
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8497
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8498
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8498
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8499
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8499
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8500
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8500
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8501
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8501
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8502
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8502
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8503
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8503
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8504
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8504
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8505
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8505
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8506

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8506
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8507
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8507
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atgaaagcat tgcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8508
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8508
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Leu Asp Glu Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8509
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8509
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8510
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8510
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8511

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8511
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8512
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8512
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8513
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8513
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8514
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8514
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160

Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8515
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8515
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360

attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8516
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8516
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu

210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8517
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8517
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780

ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8518
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8518
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270

Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8519
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8519
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200

ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8520
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8520
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys

325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8521
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8521
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atagaagcat ttcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8522
<211> 457

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8522
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380

Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ser Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8523
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8523
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8524
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8524

Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu

435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8525
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8525
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8526
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8526
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe

50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8527
<211> 1371

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8527
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8528
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8528
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110

Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8529
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8529

atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8530
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8530
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu

165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8531
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8531
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420

ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg tatattgaag atgaagttgg atgaaagcat tgcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8532
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8532
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220

Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Met Lys
420 425 430
Leu Asp Glu Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8533
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8533
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840

ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8534
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8534
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro

275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8535
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8535
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagtcgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260

gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8536
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8536
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335

Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8537
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8537
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag atgaagttgg atgaaagcct tgcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8538
<211> 457
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8538
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly

385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Met Lys
420 425 430
Leu Asp Glu Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8539
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8539
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8540
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8540
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu

1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445

Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8541
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8541
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag atgaagttgg atagaagcat ttcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8542
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8542
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60

Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Met Lys
420 425 430
Leu Asp Arg Ser Ile Ser Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8543
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8543
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg tatattgaag atgaagttgg atataagcct tgcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8544
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8544
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Met Lys
420 425 430
Leu Asp Ile Ser Leu Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8545
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8545
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8546
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8546
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8547
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8547
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480

ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagtcgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt acgcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8548
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8548
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Thr Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8549
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8549
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg cagattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900

agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg tatattgaag gataagttgg atgaaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8550
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8550
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Gln Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Asp Lys
420 425 430
Leu Asp Glu Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8551
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8551
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8552
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8552
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8553
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8553
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8554
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8554
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8555
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8555
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8556
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8556
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 8557
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8557
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8558
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8558
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8559
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8559
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcctg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8560
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8560
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8561
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8561
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120

gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8562
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8562
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala

180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8563
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8563
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540

ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg tatattgaag atgaagttgg atgaaagcat tgcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8564
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8564
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240

Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Ile Leu Lys Met Lys
420 425 430
Leu Asp Glu Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8565
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8565
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960

gagtcgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8566
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8566
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser

290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Ser Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8567
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8567
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8568
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8568
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350

Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8569
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8569
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8570
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8570
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp

405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8571
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8571
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8572
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8572
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala

20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8573
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8573
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8574
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8574
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80

His Gly Pro Gly Ala Gly Lys Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8575
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8575
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8576
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8576
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met

130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8577
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8577
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180

cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8578
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8578
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190

Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8579
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8579
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600

ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8580
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8580
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu

245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8581
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8581
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020

caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgcgcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8582
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8582
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300

Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8583
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8583
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagttgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8584
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8584
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly

355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8585
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8585
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8586
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8586
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415

Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8587
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8587
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagaggcag gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8588
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8588
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30

Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Ala Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8589
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8589
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8590
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8590
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly

85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8591
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8591
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaact gtcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8592
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8592
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Cys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140

Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8593
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8593
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240

catggtccgg gcgcgggtaa gagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctgc aaaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8594
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8594
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Lys Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Gln
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu

195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8595
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8595
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg ctgattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagctcg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660

tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcctggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8596
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8596
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Leu Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255

Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Leu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8597
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8597
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcaccg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080

accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8598
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8598
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Thr Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile

305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8599
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8599
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtgc aagaatcccg cagattaaca aacacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgttcaac gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggataccgat 780
ccgagcgttg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaggtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8600
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8600
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Ala Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Gln Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Thr Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365

Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8601
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8601
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagccggagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct catgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8602
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8602
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Pro Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys

420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8603
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8603
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccggaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagacggagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccagtggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8604
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8604
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn

35 40 45
Phe Asn Ala Pro Glu Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Gln Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8605
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8605
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgctccg cagccggagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct catgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgt tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccattggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8606
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8606
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Ala Pro Gln Pro Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95

Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8607
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8607
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagccggagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccagtggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8608
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8608
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Pro Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe

145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Gln Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8609
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8609
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300

cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccagtggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8610
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8610
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Gln Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205

Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8611
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8611
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagccggagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct catgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccagtggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720

ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8612
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8612
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Pro Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Gln Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro

260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8613
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8613
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagccggagt ggcttagcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140

ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8614
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8614
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Pro Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320

Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8615
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8615
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagccggagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaggagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcactatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccggcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8616

<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8616
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Pro Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Arg Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala

370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8617
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8617
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccattggaa agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8618
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8618
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Lys Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430

Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8619
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8619
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtacag cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagccggagt ggcttagcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct catgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgagcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa agaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8620
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8620
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Ser Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45

Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Pro Glu Trp Leu Ser Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Ser Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8621

<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8621
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg cagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
actggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcct catgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccagtggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 8622
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8622
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
Thr Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Leu Met Arg Asp Ser Pro

100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser Gln Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 8623
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8623
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8624
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8624
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8625
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8625
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagacccttc aaaatcttaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8626
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8626
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Thr
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8627
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8627
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgtcagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8628
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8628
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8629
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8629
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgtgagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8630
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8630
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8631
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8631
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacttcagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8632
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8632
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8633
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8633
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagacccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8634
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8634

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Thr
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 8635
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8635
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagaaccttc aaaatcttaa gccagatctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8636
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8636
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg

50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Asn
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8637
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8637
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgtgagc aagacccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattagcgg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8638
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8638
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Thr
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8639
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8639

atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgtcagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgattggcgg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8640
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8640
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Gly Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8641
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8641
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacttgagc aagacccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8642
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8642
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Leu Ser Lys Thr
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8643
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8643
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgtcagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8644
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8644
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8645
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8645
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgtgagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtct cgcttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8646
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8646
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ser Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8647
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8647
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagaaccttc aaaatcttaa gccagatctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaacgcaa cgcctacaag 1350

<210> 8648
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8648
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Asn
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8649
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8649
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaacgcaa cgcctacaag 1350

<210> 8650
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8650
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 8651
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8651
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtct cgcttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8652
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8652
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ser Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8653
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8653
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacgttagc aagatccttc aagcgcttaa ggtcgatctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtacgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8654
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8654
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Val Ser Lys Ile
100 105 110
Leu Gln Ala Leu Lys Val Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8655
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8655
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagaaccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaacgcaa cgcctacaag 1350

<210> 8656
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8656
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Asn
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8657
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8657
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca ggaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caacttcagc aagaaccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8658
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8658
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Arg
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Asn
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu

225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8659
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8659
atgcaccatc atcatgaagg cgtgagcggc ctgaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaacgcaa cgcctacaag 1350

<210> 8660
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8660
Met His His His His Glu Gly Val Ser Gly Leu Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Lys Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8661
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8661
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtggaagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagaaccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8662
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8662
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Gly Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Asn
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8663
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8663
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcggtatgt atttagttag caccgccatt aatctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8664
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8664
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Gly Met Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8665
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8665
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttaacgag caccgccatt caactcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8666
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8666
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Thr Ser Thr
35 40 45
Ala Ile Gln Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 8667
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8667
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
cccgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8668
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8668
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Pro Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8669
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8669
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
cccgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8670
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8670
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Pro Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8671
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8671
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aatctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
ggtgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8672
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8672
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Gly Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu

180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8673
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8673
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccgctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8674
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8674
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240

Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8675
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8675
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt acactgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
tccgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8676
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8676
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ser Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8677
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8677
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt acactggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8678
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8678
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8679
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8679
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt acactggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccgctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8680
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8680
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8681
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8681
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8682
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8682
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8683
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8683
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaaa 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
ggtgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8684
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8684
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Gly Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8685
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8685
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt acactggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
cccgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8686
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8686
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Pro Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8687
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8687
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaaa 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
tccgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccgctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8688
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8688
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ser Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190

Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8689
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8689
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt acactgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
ggtgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8690
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8690
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Gly Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8691
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8691
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
cccgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8692
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8692
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Pro Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8693
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8693
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aatctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccgctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8694
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8694
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8695
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8695
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
tccgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8696
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8696
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ser Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8697
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8697
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
tccgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8698
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8698
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ser Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8699
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8699
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttacttaa caccgccatt caactcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8700
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8700
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Leu Asn Thr
35 40 45
Ala Ile Gln Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8701
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8701
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgctatcc atttagttag caccgccatt aatctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt acactgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8702
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8702
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Ala Ile His Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8703
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8703
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
ggtgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagccgctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8704
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8704
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Gly Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Pro Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8705
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8705
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttaa caccggcatt aatctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8706
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8706
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Asn Thr
35 40 45
Gly Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8707
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8707
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttaa caccgccatt gtgctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcac tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8708
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8708
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Asn Thr
35 40 45
Ala Ile Val Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8709
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8709
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aatctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt acactgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaacctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8710
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8710
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Thr Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8711
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8711
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttacgt atttagttag caccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctgcatc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
cccgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8712
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8712
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Thr Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu His Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Pro Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8713
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8713
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacct cccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8714
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8714
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Leu Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8715
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8715
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tacgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8716
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8716
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Thr Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8717
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8717
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8718
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8718
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8719
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8719
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccatctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8720
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8720
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8721
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8721
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720

gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8722
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8722
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8723
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8723
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8724
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8724
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8725
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8725
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8726

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8726
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8727
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8727
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat taggcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8728
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8728
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Arg Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8729
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8729
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacat gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8730
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8730
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Met Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8731

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8731
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacttt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8732
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8732
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Phe Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8733
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8733
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt cccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8734
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8734
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8735
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8735
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360

gtcctttacg attttctgat accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8736
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8736
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8737
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8737
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacct caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8738
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8738
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Leu Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8739
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8739
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgcaagtc 1200

ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8740
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8740
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8741
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8741
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacttt 1260
agcaaacggc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8742
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8742
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Phe Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8743
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8743
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tacgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8744
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8744

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Thr Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 8745
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8745
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8746
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8746
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8747
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8747
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tacgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8748
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8748
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Thr Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8749
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8749

atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccatctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8750
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8750
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile His Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8751
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8751
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8752
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8752
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8753
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8753
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8754
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8754
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8755
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8755
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt cccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat taagcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8756
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8756
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Lys Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8757
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8757
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8758
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8758
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8759
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8759
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8760
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8760
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 8761
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8761
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8762
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8762
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8763
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8763
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgat accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8764
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8764
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ile Pro

115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8765
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8765
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8766
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8766
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8767
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8767
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt caacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8768
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8768
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu

225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8769
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8769
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccatctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8770
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8770
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8771
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8771
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttatgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8772
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8772
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Met Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8773
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8773
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccatctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt cccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8774
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8774
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8775
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8775
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8776
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8776
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 8777
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8777
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8778
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8778
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8779
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8779
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt cccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8780
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8780
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125

Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8781
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8781
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tatgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8782
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8782
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu

180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Met Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8783
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8783
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat taggaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8784
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8784
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240

Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Arg Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8785
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8785
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt cccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttagtga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8786
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8786
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Ser Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8787
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8787
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8788
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8788
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8789
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8789
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8790
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8790
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8791
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8791
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacag caactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacttt 1260
agcaaactgc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8792
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8792
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ser Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Phe Ser Lys Leu Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8793
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8793
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttcctgca atccgtctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgcaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8794
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8794
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8795
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8795
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttgaagca atccatctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt cccgtttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tctgaaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacttt 1260
agcaaactgc tgagagcgag ccgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 8796
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8796
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Glu Ala Ile His Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Pro
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Leu Lys Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Phe Ser Lys Leu Leu Arg Ala Ser Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 8797
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8797
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180

tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8798
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8798
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8799
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8799
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8800
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8800
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8801
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8801
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8802
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8802
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8803
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8803
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8804
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8804
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8805
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8805
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8806
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8806
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8807
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8807
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8808
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8808
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8809
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8809
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8810
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8810
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8811
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8811
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440

ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8812
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8812
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8813
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8813
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8814
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8814
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8815
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8815
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800

gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8816
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8816
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8817
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8817
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8818
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8818
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8819
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8819
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160

gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8820
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8820
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8821
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8821
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8822
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8822
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8823
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8823
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8824
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8824
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8825
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8825
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8826
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8826
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8827
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8827
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8828
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8828
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
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His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8829
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8829
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
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gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8830
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8830

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8831
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8831
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gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8832
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8832
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8833
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8833
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120

aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8834
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8834
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8835
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8835
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8836
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8836
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8837
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8837
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8838
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8838
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8839
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8839
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8840
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8840
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8841
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8841
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8842
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8842
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8843
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8843
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8844
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8844
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8845
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8845
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8846
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8846
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8847
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8847
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aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8848
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8848
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8849
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8849
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560

tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8850
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8850
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8851
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8851
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8852
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8852
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8853
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8853
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8854
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8854
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8855
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8855
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8856
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8856
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8857
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8857
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aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8858
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8858
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8859
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8859
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8860
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8860
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8861
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8861
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8862
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8862
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8863

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8863
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8864
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8864
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8865
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8865
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8866
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8866
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8867
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8867
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8868
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8868
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8869
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8869
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8870
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8870
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480

Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8871
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8871
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8872
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8872
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8873
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8873
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8874
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8874
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8875
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8875
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8876
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8876
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8877
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8877
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8878
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8878
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8879
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8879
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8880
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8880
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8881
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8881
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8882
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8882
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8883
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8883
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8884
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8884
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8885
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8885
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aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8886
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8886
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8887
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8887
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680

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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8888
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8888
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8889
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8889
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8890
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8890
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8891
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8891
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8892
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8892
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8893
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8893
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8894
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8894
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8895
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8895
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8896
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8896
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 8897
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8897
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8898

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8898
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8899
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8899
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8900
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8900
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8901
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8901
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8902
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8902
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8903
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8903
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8904
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8904
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp

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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8905
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8905

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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8906
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8906
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val

465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8907
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8907
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aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180

tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8908
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8908
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8909
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8909
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8910
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8910
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8911
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8911
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8912
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8912
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8913
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8913
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8914
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8914
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8915
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8915
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8916
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8916
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8917
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8917
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8918
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8918
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr

610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8919
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8919
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8920
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8920
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8921
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8921
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440

ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8922
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8922
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8923
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8923
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8924
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8924
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8925
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8925
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8926
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8926
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8927
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8927
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8928
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8928
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8929
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8929
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160

gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8930
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8930
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8931
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8931
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8932
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8932
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8933
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8933
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8934
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8934
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8935
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8935
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8936
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8936
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8937
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8937
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8938
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8938
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8939
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8939
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8940
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8940

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8941
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8941
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8942
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8942
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8943
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8943
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120

aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8944
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8944
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8945
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8945
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8946
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8946
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8947
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8947
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8948
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8948
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8949
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8949
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8950
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8950
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8951
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8951
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8952
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8952
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8953
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8953
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8954
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8954
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8955
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8955
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8956
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8956
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8957
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8957
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8958
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8958
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8959
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8959
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8960
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8960
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8961
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8961
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8962
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8962
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8963
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8963
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920

gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8964
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8964
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8965
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8965
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8966
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8966
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8967
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8967
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8968
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8968
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8969
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8969
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8970
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8970
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1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8971
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8971
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8972
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8972
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8973

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8973
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8974
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8974
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8975
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8975
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8976
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8976
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8977
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8977
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8978
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8978
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8979
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8979
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8980
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8980
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480

Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8981
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8981
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8982
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8982
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8983
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8983
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8984
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8984
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8985
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8985
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600

caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8986
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8986
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8987
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8987
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780

atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8988
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8988
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile

130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575

Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8989
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8989
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960

ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8990
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8990
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8991
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8991
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8992
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8992
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8993
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8993
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8994
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8994
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8995
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8995
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8996
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8996
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8997
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8997
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 8998
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8998
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255

Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp

690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 8999
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 8999
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860

atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9000
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9000
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly

275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720

Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9001
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9001
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040

gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9002
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9002
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300

Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr

740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9003
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9003
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220

tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9004
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9004
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp

325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765

Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9005
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9005
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9006
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9006
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350

Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu

785 790

<210> 9007
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9007
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9008

<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9008
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu

370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9009
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9009
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9010
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9010
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400

Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9011
<211> 2379
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9011
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9012
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9012
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr

420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9013
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9013
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9014
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9014
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp

1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445

Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9015
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9015

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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9016
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9016
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30

His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val

465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9017
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9017
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
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ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
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aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9018
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9018
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His

50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495

Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9019
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9019
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360

gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9020
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9020
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80

Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu

515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9021
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9021
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540

aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9022
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9022
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln

100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540

Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9023
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9023
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720

ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9024
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9024
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125

Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly

565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9025
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9025
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900

ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9026
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9026
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp

145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590

Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9027
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9027
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080

cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggacaatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9028
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9028
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175

His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp Asn Tyr

610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9029
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9029
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260

tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
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ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9030
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9030
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg

195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640

Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9031
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9031
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440

ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9032
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9032
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220

Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala

660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9033
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9033
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620

ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9034
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9034
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser

245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685

Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9035
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9035
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9036
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9036
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1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270

His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg

705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9037
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9037
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980

ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9038
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9038
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu

290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735

Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9039
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9039
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
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gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gtggcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160

gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9040
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9040
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320

Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser

755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9041
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9041
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340

ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9042
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9042
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg

340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780

Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9043
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9043
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9044
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9044
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365

Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9045
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9045
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9046
<211> 793
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9046
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly

385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9047
<211> 2379

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9047
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9048
<211> 793
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9048
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415

Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9049
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9049
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aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
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gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
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ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9050
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9050

Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe

435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9051
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9051
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
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cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9052
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9052
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu

20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460

Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9053
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9053
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120

aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9054
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9054
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45

Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg

485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9055
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9055
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300

ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9056
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9056
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg

65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510

Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9057
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9057
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480

actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9058
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9058
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95

Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg

530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9059
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9059
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660

cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9060
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9060
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe

115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560

Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9061
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9061
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840

gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9062
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9062
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140

Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn

580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9063
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9063
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020

cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9064
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9064
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu

165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605

Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9065
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9065
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200

aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9066
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9066
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190

Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr

625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9067
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9067
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380

gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9068
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9068
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe

210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655

Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9069
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9069
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560

tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9070
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9070
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240

Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu

675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9071
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9071
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaagccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740

tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9072
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9072
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile

260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700

Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9073
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9073
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
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ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9074
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9074
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285

Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg

725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9075
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9075
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aaaccctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100

gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9076
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9076
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Thr Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile

305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750

Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9077
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9077
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280

cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9078
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9078
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335

Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg

770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9079
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9079
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9080
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9080
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser

355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9081
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9081
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cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9082
<211> 793

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9082
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380

Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9083

<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9083
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9084
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9084
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu

405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9085
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9085
atgattgaag aactgcgcca acagctgctg gatagcccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagatg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9086
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9086
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430

Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9087
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9087
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9088
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9088
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asn Pro Arg Ser Trp
1 5 10 15

Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile

450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9089
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9089
atgattgaag aactgcgcca acagctgctg gataacccgc gttcatggcg tgcattcctg 60

cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
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attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
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cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9090
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9090
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Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro

35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480

Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9091
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9091
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aaaacgtttc gcgcgcagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240

ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccagcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aagagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtgcaga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgtgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgttgctt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgtcgta ccgatggag 2379

<210> 9092
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9092
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60

Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser

500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gln Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Val Val Pro Met Glu
785 790

<210> 9093
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9093
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tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttaaaagac 420

gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcaccca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc aaaagaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
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aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatcc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagtctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
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gatgtggaaa atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9094
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9094
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Ser Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Ala Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu

85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Lys Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Thr
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Pro Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525

Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9095
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9095
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<210> 9096
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9096
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His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110

Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Gln Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
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145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
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Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
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465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
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Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
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Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro

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Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
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Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
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Val Val Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
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Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
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Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
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Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
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Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9097
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9097
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<400> 9098
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
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145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
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His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
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Phe Asp Ser Leu Arg Gln Ala Val Gln Tyr Leu Gly Thr Leu Pro Lys
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
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Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
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Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
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Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
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Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
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Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
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Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
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Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
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Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
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Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9099
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

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<210> 9100
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9100
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His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
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Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
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100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
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Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160

Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Glu Asn Ser Met Asp Ala

595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Met Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Cys Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9101
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9101
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cgtcatttag tcgaatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcatgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcggaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140

tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320
gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaacgcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
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gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
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gtcgcgggcg aattgtatcg tgtagtggcg gatggacgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9102
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9102
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Glu Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Met
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp

180 185 190
Phe Asp Ser Leu Arg Arg Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Arg Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620

Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9103
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9103
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aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggcttagg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagagcacca ttggtgatgg tcttacccat ctgaatcgtg cattagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcaaaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
ttgattgcga cccgtttaat cccggaaagt gatggcacga cttgtgacca gcgtctggag 1020
cctgtccatg gtgccgagaa tgtgcagatt ctgcgcgttc cgtttcgcta tgaggatggt 1080
cgtattcacc cgcattggat ctcacgcttc aaggtttggc cgtatcttga acgctatgca 1140
tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
tgcaacattg cacatgccct ggagaaaagc aagtacctgt attccgatct gcattggccg 1320

gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500
attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtatctgt ggccagaaat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatcgtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc taaagccgta ccgatggag 2379

<210> 9104
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9104
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Leu Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Ser Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg Ala Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Gln Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205

Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg
225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu Tyr Ser Asp Leu His Trp Pro Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Tyr Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Arg Arg Gly Val Phe

645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670
Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala Lys Ala Val Pro Met Glu
785 790

<210> 9105
<211> 2379
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9105
atgattgaag aactgcgcca acagctgctg gatgatccgc gttcatggcg tgcattcctg 60
cgtcatttag tcgcatctca gcgtgactca tggttacata cggatttaca gcgcgcgtgc 120
aaaacgtttc gcgaacagcc tccggaaggc tatcccgaag atattggttg gctggcagat 180
tttgtggcac atacccagga agcgatcttc cgggatccgt ggatggtttt tgcgtggcgt 240
ctacgtccag gtgtttggga gtatgtgcgc atacatgtag aacagctggc ggtggaggag 300
ctgagcactg atgaatatct gcaagccaaa gaacaacttg ttggctttgg tgcagaaggt 360
gaagctgttc tgacggtgga tttcgaagat tttcgtccgg tgagccgtcg tttacgcgac 420
gagaacacca ttggtgatgg tcttacccat ctgaatcgtc atttagcagg tcgcatctgg 480
actgatttag cagcaggtcg tagtcagatt ctggaatttc tgggcctgca tcgtctggat 540
aaccagaatc tgatgctgag caacggcaat accgattttg actctttacg tcggaccgta 600
caatatctgg gcaccttacc acgtgaaact ccgtgggcag agtttcgtga agacatgcgt 660
cgtcgtggtt ttgaacccgg ttggggcaac accgcgggcc gtgttcgcga aaccatgcgt 720
ctgctgatgg atctgcttga ctctccgagc ccagctgccc tggagagctt cctggatcgc 780
atcccgatga ttagcaacgt tctgatcgtg agcattcacg gatggtttgc gcaggacaag 840
gttctgggtc gtccggacac tggtggtcag gtcgtgtata ttctggatca ggcccgtgca 900
ctggaacgcg aaatgcgtaa ccgcctgcgc caacagggtg ttgatgtgga gccgcgcatt 960
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tcagatctgg aacgcgaagt taaggccgaa ttaggtagtc gtccagatct gatcatcggc 1200
aactatagcg acggtaatct ggttgcaacc ctgctgtcag aaaaattagg tgttacgcag 1260
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gatcacgaac aggaccatca ctttgcgtgt cagtttaccg cggatctgat cgcgatgaat 1380
gcagcagaca tcatcgtgac gagcacatac caggaaattg caggtaatga ccgcgaggtt 1440
ggtcaatatg aatctcacca ggactatact ttaccgggct tgtatcgtgt cgagaatggt 1500

attgacgtgt tcgatagcaa gtttaacatt gtgagtccgg gcgcagatgc gcgcacgtat 1560
tttagctatg cccgtactga agaacgcttc tcgtctctgt ggccagaaat cgaaagcctg 1620
ctgtttggcc gcgaaccagg tccggatatt cgtggtgttc tcgaagatcg ccagaaaccg 1680
attattctgt cgatggcccg tatggatcgc atcaagaacc tgagcggtct ggccgaactg 1740
tatggtcgga gttctcgctt acgtagcctg gccaatttgg tgatcatcgg tggtcatgtt 1800
gatgtgggga atagtatgga tgcagaagaa cgcgaagaaa tccgtcgtat gcacgagatc 1860
atggaccatt accagctgga tggtcagctg cgttgggtgg gatcgcagct ggataaaacc 1920
gtcgcgggcg aattgtatcg tgtagtggcg gatggtcgtg gcgtttttgt gcaaccagcc 1980
ctgtttgagg cgttcggcct gaccgtgatt gaggcaatga gcagtggcct gccagtgttt 2040
gcgacccgcc acggtggtcc gctggaaatc atcgaagacg gcgttagcgg cttccatatt 2100
gatcccaacg accctgaagc gaccgcagaa aaactggccg acttcctgga agcagcgcgt 2160
gaacgtccga agtattggga ggaaattagc gatgcggctc ttgcgcgcgt cagcgaacgt 2220
tacacgtggg agcgctatgc ggaacgcttg atgaccatcg cgcgtgtttt cggcttttgg 2280
cgcttcgttc tgtcacgcga atcacaggtc atggaacgct atctgcaaat gttccgccac 2340
ctgcaatggc gcccgctggc tcatgccgta ccgatggag 2379

<210> 9106
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9106
Met Ile Glu Glu Leu Arg Gln Gln Leu Leu Asp Asp Pro Arg Ser Trp
1 5 10 15
Arg Ala Phe Leu Arg His Leu Val Ala Ser Gln Arg Asp Ser Trp Leu
20 25 30
His Thr Asp Leu Gln Arg Ala Cys Lys Thr Phe Arg Glu Gln Pro Pro
35 40 45
Glu Gly Tyr Pro Glu Asp Ile Gly Trp Leu Ala Asp Phe Val Ala His
50 55 60
Thr Gln Glu Ala Ile Phe Arg Asp Pro Trp Met Val Phe Ala Trp Arg
65 70 75 80
Leu Arg Pro Gly Val Trp Glu Tyr Val Arg Ile His Val Glu Gln Leu
85 90 95
Ala Val Glu Glu Leu Ser Thr Asp Glu Tyr Leu Gln Ala Lys Glu Gln
100 105 110
Leu Val Gly Phe Gly Ala Glu Gly Glu Ala Val Leu Thr Val Asp Phe
115 120 125
Glu Asp Phe Arg Pro Val Ser Arg Arg Leu Arg Asp Glu Asn Thr Ile
130 135 140
Gly Asp Gly Leu Thr His Leu Asn Arg His Leu Ala Gly Arg Ile Trp
145 150 155 160
Thr Asp Leu Ala Ala Gly Arg Ser Gln Ile Leu Glu Phe Leu Gly Leu
165 170 175
His Arg Leu Asp Asn Gln Asn Leu Met Leu Ser Asn Gly Asn Thr Asp
180 185 190
Phe Asp Ser Leu Arg Arg Thr Val Gln Tyr Leu Gly Thr Leu Pro Arg
195 200 205
Glu Thr Pro Trp Ala Glu Phe Arg Glu Asp Met Arg Arg Arg Gly Phe
210 215 220
Glu Pro Gly Trp Gly Asn Thr Ala Gly Arg Val Arg Glu Thr Met Arg

225 230 235 240
Leu Leu Met Asp Leu Leu Asp Ser Pro Ser Pro Ala Ala Leu Glu Ser
245 250 255
Phe Leu Asp Arg Ile Pro Met Ile Ser Asn Val Leu Ile Val Ser Ile
260 265 270
His Gly Trp Phe Ala Gln Asp Lys Val Leu Gly Arg Pro Asp Thr Gly
275 280 285
Gly Gln Val Val Tyr Ile Leu Asp Gln Ala Arg Ala Leu Glu Arg Glu
290 295 300
Met Arg Asn Arg Leu Arg Gln Gln Gly Val Asp Val Glu Pro Arg Ile
305 310 315 320
Leu Ile Ala Thr Arg Leu Ile Pro Glu Ser Asp Gly Thr Thr Cys Asp
325 330 335
Gln Arg Leu Glu Pro Val His Gly Ala Glu Asn Val Gln Ile Leu Arg
340 345 350
Val Pro Phe Arg Tyr Glu Asp Gly Arg Ile His Pro His Trp Ile Ser
355 360 365
Arg Phe Lys Val Trp Pro Tyr Leu Glu Arg Tyr Ala Ser Asp Leu Glu
370 375 380
Arg Glu Val Lys Ala Glu Leu Gly Ser Arg Pro Asp Leu Ile Ile Gly
385 390 395 400
Asn Tyr Ser Asp Gly Asn Leu Val Ala Thr Leu Leu Ser Glu Lys Leu
405 410 415
Gly Val Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Ser Lys Tyr
420 425 430
Leu His Ser Asp Leu His Trp Arg Asp His Glu Gln Asp His His Phe
435 440 445
Ala Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn Ala Ala Asp Ile
450 455 460
Ile Val Thr Ser Thr Tyr Gln Glu Ile Ala Gly Asn Asp Arg Glu Val
465 470 475 480
Gly Gln Tyr Glu Ser His Gln Asp Tyr Thr Leu Pro Gly Leu Tyr Arg
485 490 495
Val Glu Asn Gly Ile Asp Val Phe Asp Ser Lys Phe Asn Ile Val Ser
500 505 510
Pro Gly Ala Asp Ala Arg Thr Tyr Phe Ser Tyr Ala Arg Thr Glu Glu
515 520 525
Arg Phe Ser Ser Leu Trp Pro Glu Ile Glu Ser Leu Leu Phe Gly Arg
530 535 540
Glu Pro Gly Pro Asp Ile Arg Gly Val Leu Glu Asp Arg Gln Lys Pro
545 550 555 560
Ile Ile Leu Ser Met Ala Arg Met Asp Arg Ile Lys Asn Leu Ser Gly
565 570 575
Leu Ala Glu Leu Tyr Gly Arg Ser Ser Arg Leu Arg Ser Leu Ala Asn
580 585 590
Leu Val Ile Ile Gly Gly His Val Asp Val Gly Asn Ser Met Asp Ala
595 600 605
Glu Glu Arg Glu Glu Ile Arg Arg Met His Glu Ile Met Asp His Tyr
610 615 620
Gln Leu Asp Gly Gln Leu Arg Trp Val Gly Ser Gln Leu Asp Lys Thr
625 630 635 640
Val Ala Gly Glu Leu Tyr Arg Val Val Ala Asp Gly Arg Gly Val Phe
645 650 655
Val Gln Pro Ala Leu Phe Glu Ala Phe Gly Leu Thr Val Ile Glu Ala
660 665 670

Met Ser Ser Gly Leu Pro Val Phe Ala Thr Arg His Gly Gly Pro Leu
675 680 685
Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro Asn Asp
690 695 700
Pro Glu Ala Thr Ala Glu Lys Leu Ala Asp Phe Leu Glu Ala Ala Arg
705 710 715 720
Glu Arg Pro Lys Tyr Trp Glu Glu Ile Ser Asp Ala Ala Leu Ala Arg
725 730 735
Val Ser Glu Arg Tyr Thr Trp Glu Arg Tyr Ala Glu Arg Leu Met Thr
740 745 750
Ile Ala Arg Val Phe Gly Phe Trp Arg Phe Val Leu Ser Arg Glu Ser
755 760 765
Gln Val Met Glu Arg Tyr Leu Gln Met Phe Arg His Leu Gln Trp Arg
770 775 780
Pro Leu Ala His Ala Val Pro Met Glu
785 790

<210> 9107
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9107
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctggc gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9108
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9108
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Ala Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9109
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9109
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtaactat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9110
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9110
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Thr

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 9111
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9111
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat gttctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9112
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9112
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Val Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9113
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9113
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gattgctgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc acggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9114
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9114
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Leu Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro

115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His His Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9115
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9115
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60

cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtccttgctg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9116
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9116
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Ala Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175

Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9117
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9117
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480

cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggttatatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9118
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9118
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Tyr Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu

225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9119
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9119
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttggtctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900

cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9120
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9120
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Gly Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285

Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9121
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9121
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttgggg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320

cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9122
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9122
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Gly Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser

340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9123
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9123
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtagcgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9124
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9124
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Ala
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400

Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9125
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9125
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttcgtg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9126
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9126
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15

Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Arg Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys

450

<210> 9127
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9127
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tcagaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9128
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9128
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu

65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gln Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9129
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9129
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg atttgctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9130
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9130
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Leu Leu Gln Pro
115 120 125

Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9131
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9131
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120

ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgt ctctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9132
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9132
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Ser
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu

180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9133
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9133
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttgttaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540

atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9134
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9134
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Val Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240

Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9135
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9135
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atggttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960

gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9136
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9136
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Trp Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu

290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9137
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9137
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctggg gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaacttttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9138
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9138
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gly Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350

Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9139
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9139
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
aagatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9140
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9140
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Lys Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys

405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9141
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9141
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat tgtctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9142
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9142
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile

20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Cys Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9143
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9143
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcctg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9144
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9144
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80

Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9145
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9145
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaaatggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9146
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9146
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Met Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val

130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9147
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9147
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180

gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
gcgatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9148
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9148
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190

Asp Phe Leu Ala Pro Gly Asn Ala Ala Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9149
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9149
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600

ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9150
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9150
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu

245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9151
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9151
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggctctgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020

atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9152
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9152
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Ser Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300

Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9153
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9153
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccggctc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9154
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9154
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro Ala Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln

355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9155
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9155
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctggt gccgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9156
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9156
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Val Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415

Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9157
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9157
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg gtctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9158
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9158
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30

Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Gly
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9159
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9159
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtaggtat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9160
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9160
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Gly
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly

85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9161
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9161
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcaca tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9162
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9162
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140

Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala His Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9163
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9163
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240

ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
aatatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtccgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9164
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9164
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Asn Ile Met Leu Met Cys Thr Ser

195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9165
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9165
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660

gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc ggctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9166
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9166
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255

Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp Arg Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9167
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9167
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggctatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080

gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9168
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9168
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Tyr Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg

305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9169
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9169
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtccttcttg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgtac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggcga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9170
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9170
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Leu Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365

Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9171
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9171
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
cttatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9172
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9172
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Leu Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met

420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9173
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9173
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtccttgtgg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9174
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9174
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr

35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Val Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9175
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9175
atgcaccatc atcatgaagg cgtgagcggc cagacccaga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9176
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9176
Met His His His His Glu Gly Val Ser Gly Gln Thr Gln Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95

Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9177
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9177
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtgcgatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9178
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9178
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys

145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ala Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9179
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9179
atgcaccatc atcatgaagg cgtgagcgac cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300

gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgt tgctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9180
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9180
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Leu
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205

Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9181
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9181
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttcgg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720

gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9182
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9182
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Ser Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg

260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9183
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9183
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgc agctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140

gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9184
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9184
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Gln
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320

Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9185
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9185
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttaatac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9186

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9186
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Asn Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile

370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9187
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9187
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtccttggtg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9188
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9188
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Gly Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430

Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9189
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9189
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtcctttctg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9190
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9190
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45

Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Ser Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9191

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9191
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacatgac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9192
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9192
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Met
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile

100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9193
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9193
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcctg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9194
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9194
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160

Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Leu Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9195
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9195
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cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360

gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgc gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagcctatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9196
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9196
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn

210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Ala Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9197
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9197
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggata tgagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780

tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9198
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9198
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Tyr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270

Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9199
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9199
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcacgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200

ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9200
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9200
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Thr Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser

325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9201
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9201
atgcaccatc atcatgaagg cgtgagcggc cagaccctgc aggtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9202
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9202
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Gln Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380

Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9203
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9203
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggccgggcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9204
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9204

Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Arg Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala

435 440 445
Tyr Lys
450

<210> 9205
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9205
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacgcttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9206
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9206
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser

50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Ala Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9207
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9207
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagcgctgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9208
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9208
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Ala Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110

Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9209
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9209

atgcaccatc atcatgaagg cgtgagcgac cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcggtgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9210
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9210
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg

165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Gly Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9211
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9211
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatattaa gccggacctg 360
gtccttaatg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420

gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9212
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9212
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Ile Lys Pro Asp Leu Val Leu Asn Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220

Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9213
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9213
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggttcggca ctgtttagct acttttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840

ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9214
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9214
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ser Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn

275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9215
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9215
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggagg ggagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260

agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9216
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9216
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Gly Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335

Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9217
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9217
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcggggcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9218
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9218
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Gly Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val

385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9219
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9219
atgcaccatc atcatgaagg cgtgagcggc cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcccggcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9220
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9220
Met His His His His Glu Gly Val Ser Gly Gln Thr Leu Arg Val Leu

1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60
Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Pro Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445

Tyr Lys
450

<210> 9221
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9221
atgcaccatc atcatgaagg cgtgagcgac cagaccctga gagtactgat gtttccgtgg 60
cttgcgctgg gtcatgttaa cccgtttttg cgtatcgcta aacaactggc cgatcgtggt 120
ttcgttatct atttagttag taccgctatt aacctcgaaa gcatcaaaaa gagaatcccg 180
gagaaataca gtaatagcat ccatctggtt gagctggcgc tgccagaatt accggaactg 240
ccaccacatt accatactac caacggttta ccaccgcatc tgaacgggac cctgcacaag 300
gcactgaaga tgagcgctcc caactttagc aagatccttc aaaatcttaa gccggacctg 360
gtcctttacg attttctgca accgtgggca gaaaaagtcg cccttgaaca gggcatcccg 420
gctgttccgg ttctaaccag tggtgcggca ctgtttagct actttttcaa cttcctgaag 480
cgaccgggtc acgagtttcc gtttccggca atccgcctgt cgaagcgaga acaggataag 540
atgcgcgaga tgtttggaac agagccgacg gaagaagatt ttttagcacc tggcaatgcc 600
ggtatcatgc tgatgtgcac gagccgcgta attgaggcta agtacctgga ctattgcacc 660
gaactgacca atgtaaaagt tgttccggtt ggtccgccat ttcaggatcc gctgaccgaa 720
gatattgacg accccgaact gattgattgg ttagatacca aacccgaaaa cagtgttgtc 780
tatgtgtcgt ttggcagcga atacttcctg agccgtgaag atatggaaga agtcgcgttc 840
ggcctggagc tgagcaacgt gaactttatc tgggttgcac gctttccgaa aggcgaagaa 900
cagaatctgg aagacgttct gccaaaaggc ttcctggaac gcgttggtga tcgtggtcgc 960
gttctggacc atctggtgcc gcaggcccat attctgaacc atccgagcac gggtggcttc 1020
atctctcatt gcggttggaa cagcgtcatg gaaagcattg atttcggcgt tccgatcatt 1080
gcgatgccga tgcagtggga tcagccgatt aacgcgagac tgcttgtgga attaggcgtg 1140
gcagtggaga tcgtgcgtga tgaagatggc cggattcacc gcggcgaaat tgcccaagtc 1200
ctgaaagatg tgatttcggg cccgactggt gagatactgc gcgcgaaagt acgcgacatt 1260
agcaaacgcc tgagagcgag acgcgaggag gaaatgaacg cagcggcgga agaactgata 1320
cagctgtgtc gcaaccgcaa cgcctacaag 1350

<210> 9222
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9222
Met His His His His Glu Gly Val Ser Asp Gln Thr Leu Arg Val Leu
1 5 10 15
Met Phe Pro Trp Leu Ala Leu Gly His Val Asn Pro Phe Leu Arg Ile
20 25 30
Ala Lys Gln Leu Ala Asp Arg Gly Phe Val Ile Tyr Leu Val Ser Thr
35 40 45
Ala Ile Asn Leu Glu Ser Ile Lys Lys Arg Ile Pro Glu Lys Tyr Ser
50 55 60

Asn Ser Ile His Leu Val Glu Leu Ala Leu Pro Glu Leu Pro Glu Leu
65 70 75 80
Pro Pro His Tyr His Thr Thr Asn Gly Leu Pro Pro His Leu Asn Gly
85 90 95
Thr Leu His Lys Ala Leu Lys Met Ser Ala Pro Asn Phe Ser Lys Ile
100 105 110
Leu Gln Asn Leu Lys Pro Asp Leu Val Leu Tyr Asp Phe Leu Gln Pro
115 120 125
Trp Ala Glu Lys Val Ala Leu Glu Gln Gly Ile Pro Ala Val Pro Val
130 135 140
Leu Thr Ser Gly Ala Ala Leu Phe Ser Tyr Phe Phe Asn Phe Leu Lys
145 150 155 160
Arg Pro Gly His Glu Phe Pro Phe Pro Ala Ile Arg Leu Ser Lys Arg
165 170 175
Glu Gln Asp Lys Met Arg Glu Met Phe Gly Thr Glu Pro Thr Glu Glu
180 185 190
Asp Phe Leu Ala Pro Gly Asn Ala Gly Ile Met Leu Met Cys Thr Ser
195 200 205
Arg Val Ile Glu Ala Lys Tyr Leu Asp Tyr Cys Thr Glu Leu Thr Asn
210 215 220
Val Lys Val Val Pro Val Gly Pro Pro Phe Gln Asp Pro Leu Thr Glu
225 230 235 240
Asp Ile Asp Asp Pro Glu Leu Ile Asp Trp Leu Asp Thr Lys Pro Glu
245 250 255
Asn Ser Val Val Tyr Val Ser Phe Gly Ser Glu Tyr Phe Leu Ser Arg
260 265 270
Glu Asp Met Glu Glu Val Ala Phe Gly Leu Glu Leu Ser Asn Val Asn
275 280 285
Phe Ile Trp Val Ala Arg Phe Pro Lys Gly Glu Glu Gln Asn Leu Glu
290 295 300
Asp Val Leu Pro Lys Gly Phe Leu Glu Arg Val Gly Asp Arg Gly Arg
305 310 315 320
Val Leu Asp His Leu Val Pro Gln Ala His Ile Leu Asn His Pro Ser
325 330 335
Thr Gly Gly Phe Ile Ser His Cys Gly Trp Asn Ser Val Met Glu Ser
340 345 350
Ile Asp Phe Gly Val Pro Ile Ile Ala Met Pro Met Gln Trp Asp Gln
355 360 365
Pro Ile Asn Ala Arg Leu Leu Val Glu Leu Gly Val Ala Val Glu Ile
370 375 380
Val Arg Asp Glu Asp Gly Arg Ile His Arg Gly Glu Ile Ala Gln Val
385 390 395 400
Leu Lys Asp Val Ile Ser Gly Pro Thr Gly Glu Ile Leu Arg Ala Lys
405 410 415
Val Arg Asp Ile Ser Lys Arg Leu Arg Ala Arg Arg Glu Glu Glu Met
420 425 430
Asn Ala Ala Ala Glu Glu Leu Ile Gln Leu Cys Arg Asn Arg Asn Ala
435 440 445
Tyr Lys
450

<210> 9223
<211> 1371
<212> DNA

<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9223
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgg atgatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 9224
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9224
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe

115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Asp Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 9225
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9225
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60

ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtttga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 9226
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9226
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175

Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Leu Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 9227
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9227
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480

ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg cagagctata ttagcagcct g 1371

<210> 9228
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9228
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser

225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Gln Ser Tyr Ile Ser Ser Leu
450 455

<210> 9229
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9229
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900

agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgg gggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 9230
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9230
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285

Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Gly Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 9231
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9231
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgccgagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320

ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 9232
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9232
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Pro Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe

340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 9233
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9233
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat acgccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 9234
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9234
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Thr Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400

Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 9235
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9235
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcactctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 9236
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9236
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15

Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Thr Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu

450 455

<210> 9237
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9237
atgccaaaca caagccccac caccgtgcgt cgtcgtcgtg ttattctgtt tccggttccg 60
ttcccgggcc acttaaaccc gatgctgcaa ctggcgaacg tgctgtaccg tagaggtttt 120
gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccagccttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tacgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
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<210> 9238
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9238
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Ser Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr

65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125
Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Thr Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 9239
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9239
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gcgatcacca ttctgcacac caacttcaac gccccgaaaa ccggtcttta tccgcacttc 180
cagtttcgtt ttatcttgga caacgatccg cagaccgagt ggcttcgcaa cctgccgacc 240
catggtccgg gcgcgggtat gagaatcccg cagattaaca agcacggcgc ggatgaattc 300
cgtaaagagc tggaaagcgc gatgcgggat agcccgagtg acgaggaagt tgcgtgcgtg 360
attaccgatg cgctgtggta cttcgcgcaa ccggtggcgg acagcctgaa tctgaaacgt 420
ctggttctga tgaccagcag cctgtttaac ttccacgcgc tggtgtgcct gccgaaattt 480
ttagagttgg gctacctgga tccggaagat aaacatcgtc cggaggaacc ggtggtaggt 540
ttcccgatgc tgaaggttaa agatatccgt cgcgcgtata gccactggca agaagctaaa 600
ccaattctgg ataagatgat tgaagaaacc cgtgccagca gcggtgtgat ttggaacagc 660
tttaaagagc tggaggaaag cgagctggaa accgtttggc gtgaaattcc ggcgccgagc 720
ttcctgcttc cgctgccgaa gcattatagg gcgagcagca gcagcctgct ggatgaagat 780
ccgagcgtgg cccaatggct ggaccagcaa ccgccgagca gcgtgctgta cgttggcttt 840
ggcagccaga gcgaggtgga ccccaaagat ttcctggaga ttgcgcgtgg tctggttgct 900
agcaaacaaa gctttctgtg gctggttcgt ccgggcttcg tgaagggtta tgagtggatt 960
gagctgctgc cggatggttt tctgggtgaa aaaggtcgta tcgtgaagtc ttgcccgcaa 1020
caagaagtgc tggcgcacaa ggcgattggt gcgttctgga cccacggcgg ttggaacggc 1080
accatggagg ccgtgtgcga aggcgtgccg atgatcttta gcgatttcgg tctggatcag 1140
ccgctgaacg cgcgttacat gagcgaagtt ctgcatgtgg gcgtttatct ggagaacggc 1200
ttcgagcgtg gtgagatcat taacgcgatt aggcgtgtga tggttgaccc ggaaggtgag 1260
gttatgcgtc aaaacgcgcg taaattgaag gataagttgg atcgaagcat tgctcccggt 1320
ggcagcagct acgagagcct ggaacgcctg gttagctata ttagcagcct g 1371

<210> 9240
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> "Variant of ADP-beta-1,3-glucosyltransferase"

<400> 9240
Met Pro Asn Thr Ser Pro Thr Thr Val Arg Arg Arg Arg Val Ile Leu
1 5 10 15
Phe Pro Val Pro Phe Pro Gly His Leu Asn Pro Met Leu Gln Leu Ala
20 25 30
Asn Val Leu Tyr Arg Arg Gly Phe Ala Ile Thr Ile Leu His Thr Asn
35 40 45
Phe Asn Ala Pro Lys Thr Gly Leu Tyr Pro His Phe Gln Phe Arg Phe
50 55 60
Ile Leu Asp Asn Asp Pro Gln Thr Glu Trp Leu Arg Asn Leu Pro Thr
65 70 75 80
His Gly Pro Gly Ala Gly Met Arg Ile Pro Gln Ile Asn Lys His Gly
85 90 95
Ala Asp Glu Phe Arg Lys Glu Leu Glu Ser Ala Met Arg Asp Ser Pro
100 105 110
Ser Asp Glu Glu Val Ala Cys Val Ile Thr Asp Ala Leu Trp Tyr Phe
115 120 125

Ala Gln Pro Val Ala Asp Ser Leu Asn Leu Lys Arg Leu Val Leu Met
130 135 140
Thr Ser Ser Leu Phe Asn Phe His Ala Leu Val Cys Leu Pro Lys Phe
145 150 155 160
Leu Glu Leu Gly Tyr Leu Asp Pro Glu Asp Lys His Arg Pro Glu Glu
165 170 175
Pro Val Val Gly Phe Pro Met Leu Lys Val Lys Asp Ile Arg Arg Ala
180 185 190
Tyr Ser His Trp Gln Glu Ala Lys Pro Ile Leu Asp Lys Met Ile Glu
195 200 205
Glu Thr Arg Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu
210 215 220
Glu Glu Ser Glu Leu Glu Thr Val Trp Arg Glu Ile Pro Ala Pro Ser
225 230 235 240
Phe Leu Leu Pro Leu Pro Lys His Tyr Arg Ala Ser Ser Ser Ser Leu
245 250 255
Leu Asp Glu Asp Pro Ser Val Ala Gln Trp Leu Asp Gln Gln Pro Pro
260 265 270
Ser Ser Val Leu Tyr Val Gly Phe Gly Ser Gln Ser Glu Val Asp Pro
275 280 285
Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Ala Ser Lys Gln Ser
290 295 300
Phe Leu Trp Leu Val Arg Pro Gly Phe Val Lys Gly Tyr Glu Trp Ile
305 310 315 320
Glu Leu Leu Pro Asp Gly Phe Leu Gly Glu Lys Gly Arg Ile Val Lys
325 330 335
Ser Cys Pro Gln Gln Glu Val Leu Ala His Lys Ala Ile Gly Ala Phe
340 345 350
Trp Thr His Gly Gly Trp Asn Gly Thr Met Glu Ala Val Cys Glu Gly
355 360 365
Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala
370 375 380
Arg Tyr Met Ser Glu Val Leu His Val Gly Val Tyr Leu Glu Asn Gly
385 390 395 400
Phe Glu Arg Gly Glu Ile Ile Asn Ala Ile Arg Arg Val Met Val Asp
405 410 415
Pro Glu Gly Glu Val Met Arg Gln Asn Ala Arg Lys Leu Lys Asp Lys
420 425 430
Leu Asp Arg Ser Ile Ala Pro Gly Gly Ser Ser Tyr Glu Ser Leu Glu
435 440 445
Arg Leu Val Ser Tyr Ile Ser Ser Leu
450 455